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OM protein - protein search, using sw model

Run on: August 6, 2003, 09:30:44 ; Search time 84 Seconds  
(without alignments)  
345.797 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEFGATVLLFLP.....RRRSQSPRRRSQSRQSC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03.\*

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3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	971	100.0	183	18 AAW09044	Hepatitis B virus
2	956	98.5	183	20 AAY29674	Human hepatitis B
3	956	98.5	183	23 ABG94182	Hepatitis B capsid
4	956	98.5	183	23 ABG80494	Hepatitis B virus
5	956	98.5	183	23 AAU93961	Hepatitis B virus
6	956	98.5	183	23 AAU87796	Human hepatitis B
7	956	98.5	183	23 AAU80906	Hepatitis B virus
8	956	98.5	194	19 AAW50242	Hepatitis B virus
9	956	98.5	212	19 AAW50250	Hepatitis B virus

10	956	98.5	212	23 AAE19793	Hepatitis B virus
11	956	98.5	212	23 AAE19898	Hepatitis B virus
12	956	98.5	212	23 AAE17018	Hepatitis B virus
13	956	98.5	346	13 AAR27473	SL2/core protein.
14	954	98.2	183	23 ABG94185	Hepatitis B capsid
15	954	98.2	183	23 ABG80497	Hepatitis B virus
16	954	98.2	183	23 ABG80909	Hepatitis B capsid
17	953	98.1	183	23 ABG94187	Hepatitis B capsid
18	953	98.1	183	23 ABG94188	Hepatitis B virus
19	953	98.1	183	23 ABG80499	Hepatitis B virus
20	953	98.1	183	23 ABG80500	Hepatitis B virus
21	953	98.1	183	23 AAU80911	Hepatitis B virus
22	953	98.1	183	23 AAU80912	HBV genotype D pre
23	953	98.1	212	22 AAG66924	Hepatitis B capsid
24	953	98.1	212	23 ABG94190	Hepatitis B capsid
25	953	98.1	212	23 ABG94191	Hepatitis B capsid
26	953	98.1	212	23 ABG94192	Hepatitis B virus
27	953	98.1	212	23 ABG80502	Hepatitis B virus
28	953	98.1	212	23 ABG80503	Hepatitis B virus
29	953	98.1	212	23 ABG80504	Hepatitis B virus
30	953	98.1	212	23 AAU80914	Hepatitis B virus
31	953	98.1	212	23 AAU80915	Hepatitis B virus
32	953	98.1	212	23 AAU80916	Hepatitis B virus
33	951	97.9	212	23 ABG94195	Hepatitis B capsid
34	951	97.9	212	23 ABG94196	Hepatitis B capsid
35	951	97.9	212	23 ABG94197	Hepatitis B capsid
36	951	97.9	212	23 ABG80507	Hepatitis B virus
37	951	97.9	212	23 ABG80508	Hepatitis B virus
38	951	97.9	212	23 ABG80509	Hepatitis B virus
39	951	97.9	212	23 AAU80919	Hepatitis B virus
40	951	97.9	212	23 AAU80920	Hepatitis B virus
41	951	97.9	212	23 AAU80921	Hepatitis B virus
42	950	97.8	212	23 ABG94198	Hepatitis B capsid
43	950	97.8	212	23 ABG94199	Hepatitis B capsid
44	950	97.8	212	23 ABG94200	Hepatitis B capsid
45	950	97.8	212	23 ABG80510	Hepatitis B virus

#### ALIGNMENTS

RESULT 1

AAW09044

ID AAW09044 standard; Protein; 183 AA.

XX AC AAW09044;

XX AC AAW09044;

DT 11-APR-1997 (first entry)

XX Hepatitis B virus core protein.

DE Hepatitis B virus core protein.

XX Hepatitis B virus core protein.

KW Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus;

KW ground squirrel hepatitis B virus; duck hepatitis B virus;

KW core protein; replication; antiviral; gene therapy.

XX Hepatitis B virus.

OS Hepatitis B virus.

XX Key Location/Qualifiers

FT Misc-difference 71..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 71-180 in mutant

FT polypeptides of the invention (Claim 23);"

FT Misc-difference 81..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 81 and 180 in mutant

FT polypeptides of the invention (Claim 5);"

FT Misc-difference 171..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 171 and 180 in mutant

FT polypeptides of the invention (Claim 6);"

FT Misc-difference 174..180

FT /note= "C-terminus of core protein is at any amino

FT acid position between 174 and 180 in mutant

FT Misc-difference 178 polypeptides of the invention (Claim 26)"  
 FT AC /note- "C-terminus of core protein is at amino acid  
 FT DT position 178 in mutant polypeptides of the  
 FT DE invention (Claim 7)"  
 FT XX  
 FT Misc-difference 178  
 FT AC /note- "C-terminus of core protein is at amino acid  
 FT DT position 178 in mutant polypeptides of the  
 FT DE invention (Claim 7)"  
 FT XX  
 FT Misc-difference 172.183  
 FT AC /note- "amino acid residues 172-183, pref. 174-180,  
 FT DT are deleted from the core protein in mutant  
 FT DE polypeptides of the invention"  
 FT XX  
 PN WO9700698-A1.  
 XX  
 XX 09-JAN-1997.  
 PD  
 XX 20-JUN-1996; 96WO-US10602.  
 PF  
 XX 20-JUN-1995; 95US-0017814.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Melegari M, Scaglioni PP, Wands JR;  
 PI  
 XX WPI; 1997-087176/08.  
 DR  
 XX N-PSDB; AA749594.  
 DR  
 XX New method for inhibiting the replication of hepadnaviruses -  
 PT comprises introducing a mutant polypeptide with a mutated core  
 PT protein or corresponding nucleic acid, for treating, e.g. hepatitis  
 PT B

Claim 5; Page 55-56; 83pp; English.

Alteration of the C-terminus of the core protein (AAW09044) of  
 hepatitis B virus (HBV) or other hepadnavirus creates a mutant  
 polypeptide capable of reducing replication of the wild-type virus  
 by a dominant negative mechanism. The inhibitory effect is  
 species-specific and is achieved by deletion of a few C-terminal  
 amino acids from the core protein, and/or by joining the core  
 protein to a hepadnavirus surface protein (see also AAW09045),  
 creating a core-surface fusion. Such mutant polypeptides (see  
 also AAW09046-50) can be used to treat hepadnavirus, e.g. HBV,  
 infection.

Sequence 183 AA;

Query Match 100.0%; Score 971; DB 18; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-96;  
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MDIDYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 Db 1 MDIDYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYL 120  
 Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYL 120  
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGCRSPRRTPSPRRRRSQSRE 180  
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGCRSPRRTPSPRRRRSQSRE 180  
 QY 181 SOC 183  
 Db 181 SOC 183

RESULT 2

AAV29674

ID AAV29674 standard; Protein; 183 AA.

XX  
 AC AAV29674;  
 XX  
 DT 08-NOV-1999 (first entry)  
 XX  
 DE Human hepatitis B core protein.  
 XX  
 KW Human hepatitis B core protein; HBC; modified; Immunodominant;  
 KW nucleocapsid protein; vaccine; T cell epitope.  
 XX  
 OS Hepatitis B virus.  
 PN WO9940934-A1.  
 XX  
 XX 19-AUG-1999.  
 PD  
 XX 11-FEB-1999; 99WO-US03055.  
 PF  
 XX 12-FEB-1998; 98US-0074537.  
 PR  
 XX (IMMU-) IMMUNE COMPLEX CORP.  
 PA  
 XX Birkett AJ;  
 PI  
 XX WPI; 1999-527340/44.  
 DR  
 XX N-PSDB; AA208816.  
 DR  
 XX Conjugate of hepatitis B core protein, modified to increase  
 PT reactivity with haptens, used to raise antibodies against the haptens,  
 PT e.g. in vaccines  
 PT  
 PS Claim 17; Page 77-78; 128pp; English.

The present invention describes a conjugate (A) comprising a  
 strategically modified hepatitis B core (HBC) protein (I) attached to  
 a hapten, where (I) includes amino acids (aa) 10-140 of the wild type  
 HBC 183 aa sequence (given in AAV29674) and additionally has an insert  
 (II) in the region corresponding to aa's 50-100, where the insert is  
 of 1 to about 40 aa's and contains a chemically reactive aa residue  
 linked to the hapten. A vaccine containing (A) optionally in the form  
 of particles, is used to induce a protective antibody response against  
 the pathogen from which the haptens is derived, in humans or other  
 animals. These pathogens may be bacteria, viruses, rickettsia or  
 protozoa. Insertion of (II) overcomes the low reactivity of aa side  
 chains in native HBC protein, increasing the reactivity with haptens  
 and resulting in conjugates of improved immunogenicity. Modified HBC  
 can be derivatised in the form of particles by well-defined chemical  
 methods, and is unlikely to cause immunological side-effects. The  
 present sequence represents the wild type HBC protein.

Sequence 183 AA;

Query Match 98.5%; Score 956; DB 20; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDIDYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 Db 1 MDIDYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYL 120  
 Db 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLLWFHISCLTFGTETVIEYL 120  
 QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGCRSPRRTPSPRRRRSQSRE 180  
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGCRSPRRTPSPRRRRSQSRE 180  
 QY 181 SOC 183  
 Db 181 SOC 183

RESULT 3  
 ABG94182  
 ID ABG94182 standard; Protein; 183 AA.  
 XX  
 AC ABG94182;  
 XX  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Hepatitis B capsid (core) protein antigen (HBcAg) variant #11.  
 XX  
 KW Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;  
 KW cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array;  
 KW vaccine; infectious disease.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN WO200256905-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 21-JAN-2002; 2002WO-IB00166.  
 XX  
 PR 19-JAN-2001; 2001US-262379P.  
 PR 04-MAY-2001; 2001US-288549P.  
 PR 05-OCT-2001; 2001US-326998P.  
 PR 07-NOV-2001; 2001US-331045P.  
 XX  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 XX  
 PI Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;  
 PI Piossek C;  
 XX  
 DR WPI; 2002-627351/67.  
 XX  
 PT Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -  
 XX  
 PS Claim 112; Page 337-338; 441pp; English.  
 XX  
 CC This invention relates to a novel ordered and repetitive antigen array  
 CC used in the production of vaccines for infectious diseases. The  
 CC invention also discloses a composition comprising a non-natural  
 CC molecular scaffold comprising a core particle selected from a core  
 CC particle of a non-natural origin and a core particle of natural origin  
 CC and an organiser comprising at least one first attachment site, where  
 CC the organiser is connected to the core particle by at least one covalent  
 CC bond. Also disclosed is an antigen or antigenic determinant with at  
 CC least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta1-42) or its fragment and  
 CC where the second attachment site is selected from an attachment site not  
 CC naturally occurring with the antigen or antigenic determinant and an  
 CC attachment site naturally occurring with the antigen or antigenic  
 CC determinant, where the second attachment site is capable of association  
 CC through at least one non-peptide bond to the first attachment site and  
 CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitive antigen array.  
 CC The invention also comprises a coat protein capable of forming a capsid  
 CC which comprises mutant Qbeta coat proteins having an amino acid sequence  
 CC selected from five amino acid sequences fully defined in the  
 CC specification. The compounds of the invention may have antimicrobial,  
 CC antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic,  
 CC or hypoglycaemic activities and may be used in immunisation and as a  
 CC vaccine. The present sequence represents a protein sequence used to  
 CC create the compositions of the invention.  
 XX  
 SQ Sequence 183 AA;  
 XX  
 Query Match 98.5%; Score 956; DB 23; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDIDPYKEFGATVELLSFSPDFFSVRDLLDTASALYREALSPHCSPHHTALRQAIL 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MDIDPYKEFGATVELLSFSPDFFSVRDLLDTASALYREALSPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWGVNLEDPASRDLSVSYVNTNMGKPKQLLWFHISCLTFGTETVIELV 120  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 CWGELMTLATWGVNLEDPASRDLSVSYVNTNMGKPKQLLWFHISCLTFGTETVIELV 120  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTIVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTTIVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 SQC 183  
 |||||  
 Db 181 SQC 183  
 |||||  
 RESULT 4  
 ABG80494  
 ID ABG80494 standard; Protein; 183 AA.  
 XX  
 AC ABG80494;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Hepatitis B virus core capsid protein, HBcAg, variant #11.  
 KW Molecular antigen array; vaccine; antigen; antimicrobial;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;  
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN WO200256907-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 21-JAN-2002; 2002WO-IB00168.  
 XX  
 PR 19-JAN-2001; 2001US-262379P.  
 PR 04-MAY-2001; 2001US-288549P.  
 PR 05-OCT-2001; 2001US-326998P.  
 PR 07-NOV-2001; 2001US-331045P.  
 XX  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR) MAURER P.  
 PA (LECH) LECHNER F.  
 PA (ORTM) ORTMANN R.  
 PA (LUEO) LUEOEND R.  
 PA (STAU) STAUFENBIEL M.  
 PA (FREY) FREY P.  
 XX  
 PI Maurer P, Lechner F, Ortman R, Lueoend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
 XX  
 DR WPI; 2002-636514/68.  
 XX  
 PT Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -  
 XX  
 PS Claim 14; Page 314-315; 418pp; English.  
 XX  
 CC The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from:  
 CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 CC natural origin; and (ii) an organiser comprising at least one first

CC attachment site, where the organism is connected to the core particle by  
 CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 CC at least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 CC where the second attachment site is selected from: (i) an attachment site  
 CC not naturally occurring with the antigen or antigenic determinant; and  
 CC (ii) an attachment site naturally occurring with the antigen or  
 CC antigenic determinant, where the second attachment site is capable of  
 CC association through at least one non-peptide bond to the first attachment  
 CC site; and where the antigen or antigenic determinant and the scaffold  
 CC interact through the association to form an ordered and repetitive  
 CC antigen array. Also included is a process for producing a non-naturally  
 CC occurring ordered and repetitive antigen array. The composition is used  
 CC in immunisation and as a vaccine for diseases such as influenza,  
 CC graft versus host disease, IgE-mediated allergic reactions, anaphylaxis,  
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's  
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC an antigen for use in the array of the invention. The antigen is  
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a  
 CC cysteine- containing N- or C-terminal linker peptide which serves as the  
 CC attachment point to a virus like particle or bacterial protein (the  
 CC scaffold protein).  
 XX  
 XX Sequence 183 AA;

Query Match 98.5%; Score 956; DB 23; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFWHISCLTFGTVEYLV 120  
 DB 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFWHISCLTFGTVEYLV 120  
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180  
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180  
 QY 181 SQC 183  
 DB 181 SQC 183

RESULT 5  
 AAU93961  
 ID AAU93961 standard; Peptide; 183 AA.  
 XX  
 AC AAU93961;

02-JUL-2002 (first entry)

Hepatitis B virus Hbc epitope #1.

Immunogenic; hepadnavirus nucleocapsid protein; hepatitis B core; Hbc;  
 vaccine; B cell epitope; T cell epitope; immunostimulant.

Hepatitis B virus.

WO200214478-A2.

21-FEB-2002.

16-AUG-2001; 2001WO-US41759.

16-AUG-2000; 2000US-225843P.

PR 22-AUG-2000; 2000US-226867P.  
 PR 15-AUG-2001; 2001US-0930915.  
 XX (APOV-) APOVIA INC.  
 XX Birkett AJ;  
 PI  
 DR WPI; 2002-257601/30.  
 XX  
 XX Novel recombinant hepadnavirus nucleocapsid protein, termed as chimeric  
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,  
 PT Hbc immunogenic loop with linker for conjugated epitope and C-terminus  
 PT  
 PS Disclosure; Figure 7; 289pp; English.  
 XX  
 CC The invention relates to a recombinant hepadnavirus nucleocapsid protein,  
 CC i.e. a chimeric hepatitis B core (Hbc) protein (I), displaying one or  
 CC more immunogenic epitopes at the N-terminus, Hbc immunogenic loop (L) or  
 CC C-terminus, or having a heterologous linker for a conjugated epitope in  
 CC (L), and containing a Cys residue at, or near, the C-terminus that  
 CC confers enhanced stability to the particles. A vaccine comprising (I) is  
 CC useful for inducing an immune response in an inoculated host animal, by  
 CC inoculating a host animal with the vaccine, and maintaining that  
 CC inoculated animal for a time period sufficient for that animal to  
 CC develop an immune response. The immunogenic particles formed using (I)  
 CC are substantially free of binding to nucleic acids, and are most stable  
 CC than the particle formed from otherwise identical Hbc chimera that lacks  
 CC the C-terminal residue or in which a C-terminal Cys is replaced by  
 CC another residue. The chimera particles are most stable on storage in  
 CC aqueous compositions that are particles of similar sequence that lack any  
 CC C-terminal Cys residues. The chimera molecule exhibits the self-assembly  
 CC not exhibiting the nucleic acid binding of those native particles, and  
 CC excellent B cell and T cell immunogenicities. The chimera particles are  
 CC typically prepared in higher yield than similar particles that are free  
 CC of a C-terminal Cys. The particles are often far more immunogenic than  
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of  
 CC particles assembled from the chimera molecules are enhanced as compared to  
 CC similar particles assembled from chimera molecules lacking at least one  
 CC C-terminal Cys. AAU93802-AAU93997 represent immunogenic Hbc particles  
 CC amino acid sequences and related sequences of the invention.  
 XX  
 XX Sequence 183 AA;  
 Query Match 98.5%; Score 956; DB 23; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFWHISCLTFGTVEYLV 120  
 DB 61 CWGELMTLATWVGVNLEDPASRDVSVYVNTNMGKLFROLLWFWHISCLTFGTVEYLV 120  
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180  
 DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRE 180  
 QY 181 SQC 183  
 DB 181 SQC 183  
 RESULT 6  
 AAU87796  
 ID AAU87796 standard; Protein; 183 AA.  
 XX  
 AC AAU87796;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX

DE Human hepatitis B virus nucleocapsid protein #1.  
 XX  
 KW Hepatitis B virus; nucleocapsid protein; Hbc; hepatitis B virus core;  
 KW B cell epitope; T cell epitope; malaria; HIV-1; Plasmodium; protozoacide;  
 KW circumsporozoite; human immunodeficiency virus type I; human; squirrel;  
 KW woodchuck.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200213765-A2.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 16-AUG-2001; 2001WO-US25625.  
 XX  
 PR 16-AUG-2000; 2000US-225813P.  
 PR 15-AUG-2001; 2001US-0931325.  
 XX  
 XX (APOV-) APOVIA INC.  
 PA  
 PA Birkett AJ;  
 BI  
 XX  
 DR WPI; 2002-241832/29.  
 DR N-PSDB; ABK44278.  
 XX  
 XX Recombinant hepatitis B virus core protein chimera molecule, useful to  
 PT induce antibodies to malarial parasites, comprises malaria-specific  
 PT T-cell epitope and is engineered for enhanced stability -  
 XX  
 PS Disclosure: Fig 6; 197pp; English.  
 XX  
 CC The invention relates to a recombinant hepatitis B virus core (Hbc)  
 CC protein chimera molecule that contains 4 peptide-linked amino acid residue  
 CC sequence domains. The molecule of the invention contains a region  
 CC constituting a B cell epitope of the circumsporozoite protein of a  
 CC species of the parasite, Plasmodium. The chimera sequence is useful as an  
 CC immunogen for inducing antibodies to the malaria-causing parasite,  
 CC Plasmodium, particularly P. falciparum and P. vivax. Sequences  
 CC AAU87695-AAU87804 represent peptide epitopes of the invention.  
 XX  
 SQ Sequence 183 AA;  
 Query Match 98.5%; Score 956; DB 23; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDIDPKFEGATVELLSFLPSDFPSVNDLDTASALYREALSPHCSPHHTALRQAIL 60  
 DB 1 MDIDPKFEGATVELLSFLPSDFPSVNDLDTASALYREALSPHCSPHHTALRQAIL 60  
 QY 61 CWGELMTLATWGVNLEDPASRDLVSVVNTNMGKLFQLLWFHISCLTFCGTETVIEYLV 120  
 DB 61 CWGELMTLATWGVNLEDPASRDLVSVVNTNMGKLFQLLWFHISCLTFCGTETVIEYLV 120  
 QY 121 SFGWIRTPPAYRPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180  
 DB 121 SFGWIRTPPAYRPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSPRE 180  
 QY 181 SQC 183  
 DB 181 SQC 183  
 RESULT 7  
 AAU80906  
 ID AAU80906 standard; Protein; 183 AA.  
 XX  
 AC AAU80906;  
 XX  
 XX 09-APR-2002 (first entry)  
 DT  
 XX Hepatitis B virus core antigen variant (HBCag) #11.  
 DE  
 XX

KW Vaccine; molecular scaffold; pilus; pilin; HBCag; antigen;  
 KW hepatitis B virus capsid protein; JUN; FOS; HIV gp140;  
 KW measles virus N protein; bee venom phospholipase; Th type 2 T-helper;  
 KW Th; Sinbis virus E2 protein; amyloid beta; influenza M2 antigen;  
 KW human immunodeficiency virus infection; viral hepatitis; measles;  
 KW chicken pox; pneumonia; tuberculosis; syphilis; malaria; allergy;  
 KW cancer; chronic disease; arthritis; colitis; diabetes;  
 KW multiple sclerosis.  
 KW  
 XX Hepatitis B virus.  
 OS  
 XX WO200185208-A2.  
 PN  
 XX 15-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-IB00741.  
 PF  
 XX 05-MAY-2000; 2000US-202341P.  
 PR  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (SEBB/) SEBBEL P.  
 PA (DUNAN/) DUNANT N.  
 PA (BACH/) BACHMANN M.  
 PA (TISS/) TISSOT A.  
 PA (LECH/) LECHENER F.  
 XX  
 XX Sebbel P, Dunant N, Bachmann M, Tissot A, Lechener F;  
 PI WPI; 2002-055561/07.  
 XX  
 DR New composition, useful for vaccine production, comprises antigen or  
 XX antigenic determinant and non-natural molecular scaffold comprising  
 PT organizer and core particle such as bacterial pilus or pilin protein  
 PT -s  
 XX  
 XX Claim 34; Page 216-217; 287pp; English.  
 XX The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold (molecular scaffold) which comprises a core  
 CC particle such as a bacterial pilus or pilin protein, a recombinant form  
 CC of the protein, a virus-like particle or a hepatitis B virus capsid  
 CC protein (HBCag), and an organizer; and (b) an antigen or antigenic  
 CC determinant, where the molecular scaffold and antigenic determinant  
 CC interact to form an ordered and repetitive antigen array. Suitable  
 CC antigenic determinants include JUN, FOS, HIV gp140, measles virus N  
 CC protein, bee venom phospholipase, Sinbis virus E2 protein, amyloid beta  
 CC derived peptides and influenza M2 antigen. The composition (or vaccine)  
 CC is useful for immunisation, by administration to a subject, where the  
 CC administration produces an immune response, such as humoral, cellular or  
 CC protective immune response, preferably a Th type 2 T-helper (Th2)  
 CC response that is specific for the antigenic determinant. The  
 CC administration induces antibodies specific for the antigenic determinant  
 CC of a subtype corresponding to the Th2 subtype in the subject. The subject  
 CC does not generate a Th2 subtype that is specific for pilus or pilin  
 CC polypeptide or antigenic determinant. The composition is useful for the  
 CC production of vaccines for prevention of infectious diseases such as  
 CC human immunodeficiency virus, viral hepatitis, measles, chicken pox,  
 CC pneumonia, tuberculosis, syphilis, malaria, and for treating allergy,  
 CC cancer, and chronic diseases induced or accelerated by a Th1 type  
 CC immune response, such as arthritis, colitis, diabetes and multiple  
 CC sclerosis. The composition is useful to generate defined self-specific  
 CC antibodies and specific immune responses of the Th2 type and allows the  
 CC creation of highly efficient vaccines against infectious diseases, and  
 CC for treating allergy, cancer, and chronic diseases induced or accelerated  
 CC by a Th1 type immune response. The present sequence is a peptide or  
 CC protein incorporated into the compositions of the invention.  
 XX  
 SQ Sequence 183 AA;

Query Match 98.5%; Score 956; DB 23; Length 183;  
 Best Local Similarity 98.9%; Pred. No. 8.5e-95;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
Db 1 MDIDPYKFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
OY 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
Db 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180  
OY 181 SOC 183  
Db 181 SOC 183

## RESULT 8

AAW50242  
ID AAW50242 standard; Protein; 194 AA.

XX  
AC AAW50242;

XX  
DT 28-SEP-1998 (first entry)

XX  
DE Hepatitis B virus precore p22 polypeptide Met-p22.

XX  
KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;  
KW hepatocyte; liver; Met-p22.

XX  
OS Hepatitis B virus.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Protein 2..194  
ET /label- p22

XX  
PN WO9809649-A1.

XX  
PD 12-MAR-1998.

XX  
PF 03-SEP-1997; 97WO-US15500.

XX  
PR 03-SEP-1996; 96US-0025370.

XX  
PA (GEO ) GEN HOSPITAL CORP.

XX  
PI Melegari M, Scaglioni PP, Wands JR;

XX  
WPI; 1998-193325/17.

XX  
PT DNA encoding proteins which can be incorporated with wild type  
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for  
PT inhibition of viral replication, especially hepatitis B virus

XX  
PS Claim 11; Page 40; 60pp; English.

XX  
CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)  
CC protein with an added N-terminal Met residue. p22 is produced by  
CC elimination of the 19-amino acid leader peptide from the 25 kDa  
CC full-length HBV precore protein (see AAW50250). Evidence is provided  
CC that HBV replication is inhibited in the presence of high levels of  
CC HBV precore or precore-related proteins. These proteins can be  
CC incorporated into HBV nucleocapsids along with the p21 core protein  
CC (see AAW50251), which is the usual nucleocapsid component, and  
CC thereby render the nucleocapsids deficient in encapsitating HBV  
CC pregenomic RNA. Thus, over-expression of the precore proteins, or  
CC certain variants of them, leads to transdominant inhibition of HBV  
CC replication. Suitable inhibitory proteins include p25 (see AAW50250),  
CC p22, Met-p22, p18 (see AAW50236), Met-p18 (see AAW50237) and Met-p18-Het  
CC (see AAW50238). Heterologous peptides (see AAW50244-49) may be  
CC inserted into the p22 and Met-p22 polypeptides. The inhibitory  
CC proteins can be produced by recombinant methods using claimed

CC expression vectors and host cells. They can be provided exogenously  
CC to the target cells for use in inhibiting HBV replication.  
CC Alternatively, a nucleic acid construct that directs overexpression  
CC of an inhibitory protein in target cells is used for the gene  
CC therapy of HBV infection.

XX  
SQ Sequence 194 AA;

Query Match 98.5%; Score 956; DB 19; Length 194;  
Best Local Similarity 98.9%; Pred. No. 9.2e-95;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
Db 12 MDIDPYKFGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 71

OY 61 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
Db 72 CWGELMTLATWVGVLNLEDPASRDLYVSYVNTNMGKFRQLLWFHISCLTFGTETVIEYLV 131

OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 180  
Db 132 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTTPSPRRRSOSPRRRRSQSRE 191

OY 181 SOC 183  
Db 192 SOC 194

## RESULT 9

AAW50250  
ID AAW50250 standard; Protein; 212 AA.

XX  
AC AAW50250;

XX  
DT 28-SEP-1998 (first entry)

XX  
DE Hepatitis B virus precore p25 polypeptide.

XX  
KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;  
KW hepatocyte; liver; p25 protein.

XX  
OS Hepatitis B virus.

XX  
PN WO9809649-A1.

XX  
PD 12-MAR-1998.

XX  
PF 03-SEP-1997; 97WO-US15500.

XX  
PR 03-SEP-1996; 96US-0025370.

XX  
PA (GEO ) GEN HOSPITAL CORP.

XX  
PI Melegari M, Scaglioni PP, Wands JR;

XX  
WPI; 1998-193325/17.

XX  
PT DNA encoding proteins which can be incorporated with wild type  
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for  
PT inhibition of viral replication, especially hepatitis B virus

XX  
PS Claim 15; Page 35; 60pp; English.

XX  
CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)  
CC protein that is encoded by the full-length HBV precore gene.  
CC Evidence is provided that HBV replication is inhibited in the  
CC presence of high levels of HBV precore or precore-related proteins.  
CC These proteins can be incorporated into HBV nucleocapsids along  
CC with the p21 core protein (see AAW50251), which is the usual  
CC nucleocapsid component, and thereby render the nucleocapsids  
CC deficient in encapsitating HBV pregenomic RNA. Thus, over-  
CC expression of the precore proteins, or certain variants of them,

CC leads to transdominant inhibition of HBV replication. Suitable  
 CC inhibitory proteins include p25, p22 (see AAW50241), Met-p22 (see  
 CC AAW50242), p18 (see AAW50236), Met-p18 (see AAW50237) and Met-p18-Het  
 CC (see AAW50238). The inhibitory proteins can be produced by  
 CC recombinant methods using claimed expression vectors and host  
 CC cells. They can be provided exogenously to the target cells for  
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid  
 CC construct that directs overexpression of an inhibitory protein in  
 CC target cells is used for the gene therapy of HBV infection.

XX Sequence 212 AA;

Query Match 98.5%; Score 956; DB 19; Length 212;

Best Local Similarity 98.9%; Pred. NO. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 |||||  
 Db 30 MDIDPYKEFGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89  
 |||||  
 QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKQLLWFHISCLTFGTETVIELV 120  
 |||||  
 Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKQLLWFHISCLTFGTETVIELV 149  
 |||||  
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 180  
 |||||  
 Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209  
 |||||  
 QY 181 SQC 183  
 |||||  
 Db 210 SQC 212

RESULT 10

AAE19793

ID AAE19793 standard; Protein; 212 AA.

XX AAE19793;

DT 18-JUN-2002 (first entry)

DE Hepatitis B virus core antigenic protein (HBcAg).

KW Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis;  
 KW therapeutic; vaccine; acquired immune deficiency syndrome; influenza;  
 KW polio; herpes; rabies; AIDS; foot-and-mouth disease.

XX Hepatitis B virus.

OS Key Location/Qualifiers

FT Peptide 1..29

FT /label= Signal-peptide

FT Protein 30..212

FT /label= Mature\_HBc\_protein

XX WO200177158-A1.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-GB01607.

XX 07-APR-2000; 2000EP-0107118.

XX (MEDE-) MEDEVA EURO LTD.

XX Gehin A, Gilbert R, Stuart D, Rowlands D;

XX WPI; 2002-239995/29.

XX N-PSDB; AAD31509.

XX Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for  
 PT the prophylactic or therapeutic treatment of humans or animals against  
 PT e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or

PT foot-and-mouth disease

XX Disclosure; Page 24-25; 27pp; English.

XX The present invention relates to hepatitis B virus (HBV) core antigen  
 CC (HBcAg) fusion proteins and polynucleotides encoding such proteins.  
 CC Sequences of the invention are useful in methods of prophylactic or  
 CC therapeutic vaccination or to manufacture medicaments for prophylactic  
 CC or therapeutic vaccination of the human or animal body against HBV,  
 CC e.g. against viral hepatitis. They are also useful as a prophylactic  
 CC vaccine against e.g. hepatitis C virus, influenza, polio, herpes,  
 CC rabies, acquired immune deficiency syndrome (AIDS) or foot-and-mouth  
 CC disease. The present sequence is hepatitis B virus core antigenic  
 CC protein (HBcAg).

SQ Sequence 212 AA;

Query Match 98.5%; Score 956; DB 23; Length 212;

Best Local Similarity 98.9%; Pred. NO. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 |||||

Db 30 MDIDPYKEFGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89  
 |||||

QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKQLLWFHISCLTFGTETVIELV 120  
 |||||

Db 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFKQLLWFHISCLTFGTETVIELV 149  
 |||||

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 180  
 |||||

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209  
 |||||

QY 181 SQC 183  
 |||||

Db 210 SQC 212

RESULT 11

AAE19898

ID AAE19898 standard; Protein; 212 AA.

XX AAE19898;

DT 18-JUN-2002 (first entry)

XX Hepatitis B virus C antigen (HBcAg) and E antigen (HBeAg) sequence.

KW Hepatitis B virus; HBV; infection; virucide; fungicide; antibacterial;  
 KW cytostatic; immunostimulant; vaccine; ribavirin; immune response; cancer.

OS Hepatitis B virus.

XX WO200213855-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-IB01808.

XX 17-AUG-2000; 2000US-225767P.

XX 29-AUG-2000; 2000US-229175P.

XX 03-NOV-2000; 2000US-0705547.

XX (TRIP-) TRIPEP AB.

XX Sallberg M, Hultgren C;

XX WPI; 2002-241837/29.

XX Vaccine compositions for treating and preventing disease, preferably  
 PT hepatitis C virus infection, comprises ribavirin and antigen that has  
 PT epitope present in hepatitis C virus

PS Claim 11; Page 82; 120pp; English.

XX The invention relates to a composition comprising ribavirin and an

CC antigen preferably non structural 3 protein (NS3)/4A fragment of

CC hepatitis C virus (HCV) genome or a peptide or nucleic acid of HCV

CC sequence. The composition is useful for enhancing an immune response to

CC a hepatitis C antigen in humans, domestic, sport or pet species and as

CC vaccines for treating and preventing HCV infections. The composition is

CC also useful for treating viral, bacterial, fungal diseases and cancer.

CC The present sequence is Hepatitis B virus C antigen (HBCAg) and E antigen

CC (HBEAg) sequence.

XX Sequence 212 AA;

SQ

Query Match 98.5%; Score 956; DB 23; Length 212;

Best Local Similarity 98.9%; Pred. No. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

OY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFKROLLWFHISCLTFGTETVLEYLV 120

DB 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFKROLLWFHISCLTFGTETVLEYLV 149

OY 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRPGRSPRRRTSPRRRSQSRRRSQSRE 180

DB 150 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209

OY 181 SOC 183

DB 210 SOC 212

RESULT 12

AAEL7018

ID AAEL7018 standard; Protein; 212 AA.

AC AAEL7018;

XX

XX

DT 18-APR-2002 (first entry)

XX

DE Hepatitis B virus (HBV) core antigen (HBCAg).

XX

KW Hepatitis B virus; HBV; core antigen; HBCAg; immune system; typhoid;

KW prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes;

KW hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea;

KW tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS;

KW dengue fever; yellow fever; malaria; whooping cough; salmonellosis;

KW food poisoning; meningitis; gonorrhea; antiviral; antibacterial;

KW antiprotozoal.

XX

XX Hepatitis B virus.

OS

XX WO200198333-A2.

PN

XX

PD 27-DEC-2001.

XX

PF 22-JUN-2001; 2001WO-GB02817.

XX

XX 22-JUN-2000; 2000GB-0015308.

PR

PR 06-OCT-2000; 2000GB-0024544.

XX

XX (CELL-) CELTECH PHARM LTD.

PA

PI Page M, Li J, Pumpens P;

XX

XX WPI; 2002-098223/13.

DR

DR N-PSDB; AAD27422.

XX

XX

PT New proteins comprising a modified hepatitis B core antigen, useful as

PT a vaccine in prophylactic or therapeutic vaccination of the human or

PT animal body, particularly against hepatitis B virus infection

XX

PS Disclosure; Page 39-40; 40pp; English.

XX

CC The invention relates to modified proteins comprising hepatitis B virus

CC (HBV) core antigen (HBCAg) wherein one or more of the four arginine

CC repeats has been deleted and the protein comprising the C-terminal

CC cysteine of HBCAg. The deleted region may be replaced by an epitope

CC from a protein other than HBCAg, in which case the HBCAg acts as a

CC carrier to present the epitope to the immune system. This chimeric

CC protein or its nucleic acid is useful as a vaccine or in a method of

CC prophylactic or therapeutic vaccination of the human or animal body,

CC particularly against HBV. The nucleic acid encoding the protein may

CC be used in gene therapy or DNA vaccination protocols. The chimeric

CC protein or its nucleic acid may also be used as the basis of a

CC prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis

CC A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth

CC disease, polio, herpes, rabies, acquired immunodeficiency syndrome

CC (AIDS), dengue fever, yellow fever, malaria, tuberculosis, whooping

CC cough, salmonellosis, typhoid, food poisoning, diarrhoea, meningitis

CC or gonorrhoea. The present sequence is Hepatitis B virus core antigen

CC (HBCAg).

XX Sequence 212 AA;

SQ

Query Match 98.5%; Score 956; DB 23; Length 212;

Best Local Similarity 98.9%; Pred. No. 1e-94;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

OY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFKROLLWFHISCLTFGTETVLEYLV 120

DB 90 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFKROLLWFHISCLTFGTETVLEYLV 149

OY 121 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRPGRSPRRRTSPRRRSQSRRRSQSRE 180

DB 150 SFGWIRTTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 209

OY 181 SOC 183

DB 210 SOC 212

RESULT 13

AAAR27473

ID AAAR27473 standard; Protein; 346 AA.

XX

XX AAAR27473;

XX

DT 25-MAR-2003 (updated)

DT 24-FEB-1993 (first entry)

XX

XX

DE S12/core protein.

XX

KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KW vaccinia virus; 13L; promoter; NYVAC; recombinant; HBV L;

KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;

KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

KW deletion loci; recipient loci.

OS

XX Synthetic.

XX

XX Key Location/Qualifiers

FT region 1..108

FT /label S1

FT region 109..163

FT /label= S2

FT region 164..346

FT /label= Core

XX



PN W09215672-A1.

XX 17-SEP-1992.

XX 09-MAR-1992; 92WO-US01906.

XX 07-MAR-1991; 91US-0666056.

PR 11-JUN-1991; 91US-0713967.

PR 06-MAR-1992; 92US-0847951.

XX (VIRO-) VIROGENETICS CORP.

XX Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP;

PI Linbach KJ, Norton EK, Paoletti E, Perkus ME, Pincus SE;

PI Riviere M, Tartaglia J, Taylor J;

XX WPI: 1992-331718/40.

DR N-PSDB; AAQ29105.

XX Vaccine comprises recombinant, attenuated pox-virus - use for

XX vaccinating against viral infections such as rabies, hepatitis B,

XX HIV, HSV, EBV, CMV, mumps etc.

XX Disclosure; Fig 13; 456pp; English.

XX The sequence given is encoded by an expression cassette which

XX comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/

XX core) which is precisely linked to the I3L promoter derived from

XX vaccinia virus. This DNA sequence was linked to the S1 and S2

XX sequences and this fragment was used in the construction of a NYVAC

XX recombinant expressing the HBV gene. Other HBV genes were also used

XX in the construction. These were HBV M protein (small pre-S antigen,

XX spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene

XX sequences were inserted individually into three different sites of

XX NYVAC separated by from each other by large regions of vaccinia DNA

XX containing essential genes. NYVAC is a Copenhagen vaccine strain of

XX vaccinia virus which has been modified by deletion of six non-essential

XX regions of the genome encoding known or potential virulence factors.

XX The deletion loci were engineered as recipient loci for the insertion

XX of foreign genes. The spacing of the three inserted sequences ensured

XX that any recombination that did occur would lead to disruption of the

XX vaccinia genome and would cause unviable vaccinia virus. See also

XX AAQ35501-864.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 346 AA;

XX Query Match 98.5%; Score 956; DB 13; Length 346;

XX Best Local Similarity 98.9%; Pred. No. 1.9e-94;

XX Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

DB 164 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 223

QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

DB 224 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 283

QY 121 SFGVWIRTPPAYRPNAPILSTLPTTVRRRGRSPRRRTSPRRRRSQSRE 180

DB 284 SFGVWIRTPPAYRPNAPILSTLPTTVRRRGRSPRRRTSPRRRRSQSRE 343

QY 181 SQC 183

DB 344 SQC 346

RESULT 14

ABG94185

ID ABG94185 standard; Protein; 183 AA.

XX

AC ABG94185;

XX

DT

DE

KW

KW

OS

XX

PN

XX

PD

XX

XX

PF

XX

PR

PR

PR

PR

PR

PR

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PA

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PI

PI

XX

XX

DR

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PT

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PS

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CC

CC

CC

CC

10-DEC-2002 (first entry)

Hepatitis B capsid (core) protein antigen (HBcAg) variant #14.

Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;

cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;

vaccine; infectious disease.

Hepatitis B virus.

WO200256905-A2.

25-JUL-2002.

21-JAN-2002; 2002WO-IB00166.

19-JAN-2001; 2001US-262379P.

04-MAY-2001; 2001US-288549P.

05-OCT-2001; 2001US-326998P.

07-NOV-2001; 2001US-331045P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;

Plossek C;

WPI: 2002-627351/67.

Molecular antigen array used in the production of vaccines for

infectious diseases -

Claim 112; Page 340; 441pp; English.

This invention relates to a novel ordered and repetitive antigen array

used in the production of vaccines for infectious diseases. The

invention also discloses a composition comprising a non-natural

molecular scaffold comprising a core particle selected from a core

particle of a non-natural origin and a core particle of natural origin

and an organiser comprising at least one first attachment site, where

the organiser is connected to the core particle by at least one covalent

bond. Also disclosed is an antigen or antigenic determinant with at

least one second attachment site, where the antigen or antigenic

determinant is amyloid beta peptide (Abeta1-42) or its fragment and

where the second attachment site is selected from an attachment site not

naturally occurring with the antigen or antigenic determinant and an

attachment site naturally occurring with the antigen or antigenic

determinant, where the second attachment site is capable of association

through at least one non-peptide bond to the first attachment site and

where the antigen or antigenic determinant and the scaffold interact

through the association to form an ordered and repetitive antigen array.

The invention also comprises a coat protein capable of forming a capsid

which comprises mutant Qbeta coat proteins having an amino acid sequence

Query Match 98.2%; Score 954; DB 23; Length 183;

Best Local Similarity 98.4%; Pred. No. 1.4e-94;

Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

DB 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCSPHHTALRAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

DB 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKFRQLLWFHISCLTGTETVIEYLV 120

QY 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180  
 |||||  
 Db 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180  
 |||||  
 QY 181 SQC 183  
 |||||  
 Db 181 SQC 183

## RESULT 15

ABG80497  
 ID ABG80497 standard; Protein; 183 AA.

AC ABG80497;

XX 29-NOV-2002 (first entry)

DE Hepatitis B virus core capsid protein, HBcAg, variant #14.

XX Molecular antigen array; vaccine; antigen; antimicrobial;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;  
 KW graft versus host disease; IgE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.

XX Hepatitis B virus.

XX WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB00168.

XX 19-JAN-2001; 2001US-262379P.

XX 04-MAY-2001; 2001US-288549P.

XX 05-OCT-2001; 2001US-326998P.

XX 07-NOV-2001; 2001US-331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.

PA (LECH/) LECHNER F.

PA (ORTM/) ORTMANN R.

PA (LUBO/) LUBOEND R.

PA (STAU/) STAUFENBIEL M.

PA (FREY/) FREY P.

PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;

PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;

XX WPI; 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for  
 PT infectious diseases -

PS Claim 14; Page 317; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from:  
 CC (1) a core particle of a non-natural origin; and (2) a core particle of  
 CC natural origin; and (ii) an organiser comprising at least one first  
 CC attachment site, where the organiser is connected to the core particle by  
 CC at least one covalent bond; (b) an antigen or antigenic determinant with  
 CC at least one second attachment site, where the antigen or antigenic  
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and  
 CC where the second attachment site is selected from: (i) an attachment site

CC not naturally occurring with the antigen or antigenic determinant; and  
 CC (ii) an attachment site naturally occurring with the antigen or  
 CC antigenic determinant, where the second attachment site is capable of  
 CC association through at least one non-peptide bond to the first attachment  
 CC site; and where the antigen or antigenic determinant and the scaffold  
 CC interact through the association to form an ordered and repetitive  
 CC antigen array. Also included is a process for producing a non-naturally  
 CC occurring ordered and repetitive antigen array. The composition is used  
 CC in immunisation and as a vaccine for diseases such as influenza,  
 CC graft versus host disease, IgE-mediated allergic reactions, anaphylaxis,  
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic  
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's  
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,  
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's  
 CC disease, osteoporosis and infectious diseases. The present sequence is  
 CC an antigen for use in the array of the invention. The antigen is  
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a  
 CC cysteine- containing N- or C-terminal linker peptide which serves as the  
 CC attachment point to a virus like particle or bacterial protein (the  
 CC scaffold protein).

XX Sequence 183 AA;

Query Match 98.2%; Score 954; DB 23; Length 183;  
 Best Local Similarity 98.4%; Pred. No. 1.4e-94;  
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPFVSRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 |||||

Db 1 MDIDPYKEGATVELLSFLPSDFPFVSRDLDTASALYREALSEPHCSPHHTALRQAIL 60  
 |||||

QY 61 CWGELMTLATWGVNLEDPASRDLYVYVNTNMGLKFRQLLWFLHISCLTFGTETVLEYLV 120  
 |||||

Db 61 CWGELMTLATWGVNLEDPASRDLYVYVNTNMGLKFRQLLWFLHISCLTFGTETVLEYLV 120  
 |||||

QY 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180  
 |||||

Db 121 SFGWIRTPPAYPPNAPILSTLPETVVRRGSRPRRTTPSPRRRSQSPRRRSQSRE 180  
 |||||

QY 181 SQC 183

Db 181 SQC 183

Search completed: August 6, 2003, 09:43:43  
 Job time : 85 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:40:39 ; Search time 93 Seconds  
(without alignments)  
507.781 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEGATVELLSFLP.....RRRRSQPRRRSQSRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	956	98.5	212	12	Q89656 hepatitis b
2	953	98.1	183	12	Q8VBF8 hepatitis b
3	953	98.1	183	12	Q89437 hepatitis b
4	953	98.1	183	12	Q68008 hepatitis b
5	953	98.1	212	12	Q67876 hepatitis b
6	953	98.1	212	12	Q68020 hepatitis b
7	953	98.1	212	12	Q89597 hepatitis b
8	951	97.9	212	12	O11884 hepatitis b
9	951	97.9	212	12	Q68025 hepatitis b
10	951	97.9	212	12	Q68068 hepatitis b
11	950	97.8	212	12	Q68070 hepatitis b
12	950	97.8	212	12	Q67984 hepatitis b
13	950	97.8	212	12	Q68032 hepatitis b
14	948	97.6	212	12	Q9157 hepatitis b
15	948	97.6	212	12	Q91525 hepatitis b
16	948	97.6	212	12	Q91522 hepatitis b

17	948	97.6	212	12	Q91717	Q91717 hepatitis b
18	948	97.6	212	12	Q915X9	Q915X9 hepatitis b
19	948	97.6	212	12	Q910K2	Q910K2 hepatitis b
20	947	97.5	183	12	Q910W2	Q910W2 hepatitis b
21	947	97.5	183	12	Q8VBF6	Q8VBF6 hepatitis b
22	947	97.5	183	12	Q68048	Q68048 hepatitis b
23	947	97.5	183	12	Q68066	Q68066 hepatitis b
24	947	97.5	212	12	Q67872	Q67872 hepatitis b
25	947	97.5	212	12	Q68051	Q68051 hepatitis b
26	946	97.4	183	12	Q67989	Q67989 hepatitis b
27	946	97.4	212	12	Q67980	Q67980 hepatitis b
28	946	97.4	212	12	Q91701	Q91701 hepatitis b
29	946	97.4	212	12	Q915X4	Q915X4 hepatitis b
30	946	97.4	212	12	Q68014	Q68014 hepatitis b
31	946	97.4	212	12	Q68012	Q68012 hepatitis b
32	945	97.3	183	12	Q8VBF0	Q8VBF0 hepatitis b
33	945	97.3	212	12	Q910N8	Q910N8 hepatitis b
34	945	97.3	212	12	Q910U3	Q910U3 hepatitis b
35	945	97.3	212	12	Q68077	Q68077 hepatitis b
36	945	97.3	212	12	Q68010	Q68010 hepatitis b
37	945	97.3	212	12	Q915V4	Q915V4 hepatitis b
38	945	97.3	212	12	Q915Z1	Q915Z1 hepatitis b
39	945	97.3	212	12	Q68075	Q68075 hepatitis b
40	944	97.2	183	12	Q8UYJ2	Q8UYJ2 hepatitis b
41	944	97.2	183	12	Q8UYA0	Q8UYA0 hepatitis b
42	944	97.2	212	12	Q68030	Q68030 hepatitis b
43	944	97.2	212	12	Q917J5	Q917J5 hepatitis b
44	944	97.2	212	12	Q9QMH8	Q9QMH8 hepatitis b
45	944	97.2	212	12	Q96845	Q96845 hepatitis b

#### ALIGNMENTS

#### RESULT 1

Q89656 PRELIMINARY; PRT; 212 AA.  
ID Q89656  
AC Q89656;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Core antigen (Precore protein).  
GN PREC.  
OS Hepatitis B virus.  
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AYW4;  
RA Plucienniczak A.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=61012091; PubMed=399327;  
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli.";  
RL Nature 281:646-650(1979).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Borisova G.P., Pumpen P.P., Bychko V.V., Pushko P.M., Kalis Y.V.,  
RA Dishler A.V., Gren E.Y., Tsubinogin V.V., Kukain R.A.;  
RL Dokl. Biochem. 279:386-390(1985).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RA Petzold D.R., Tautz B., Wolf F., Drescher J.;  
RT "Infection chains and evolution rates of Hepatitis B Virus in cardiac transplant recipients infected nosocomially.";

RL J. Med. Virol. 0:0-0(1999).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=1;

RA Petzold D.R.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RC Kay A.C.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RN [8]

RP SEQUENCE FROM N.A.

RA Jeantet D., Chemin I., Mandrand B., Zoulim F., Trepo C., Kay A.;

RT "Characterization of two Hepatitis B virus populations isolated from a

RT Hepatitis B surface antigen-negative patient.,"

RL Hepatology 0:0-0(0).

DR EMBL; X85290; CAA59609.1; -

DR EMBL; X85300; CAA59631.1; -

DR EMBL; X85313; CAA59659.1; -

DR EMBL; X85283; CAA59593.1; -

DR EMBL; X85306; CAA59644.1; -

DR EMBL; X85316; CAA84786.1; -

DR EMBL; X85312; CAA59657.1; -

DR EMBL; AJ131956; CAA10538.1; -

DR EMBL; AJ344117; CAC87011.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

SQ SEQUENCE 212 AA; 24350 MW; D3016A4E8B05A1B8 CRC64;

Query Match 98.5%; Score 956; DB 12; Length 212;

Best Local Similarity 98.9%; Pred. No. 1.3e-89;

Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

DB 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLLWFHISCLTFFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLLWFHISCLTFFGTETVIEYL 149

QY 121 SGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

DB 150 SGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

RESULT 2

Q8VBF8

ID Q8VBF8 PRELIMINARY; PRT; 183 AA.

AC Q8VBF8:

DT 01-MAR-2002 (TREMELrel. 20, Created)

DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Core protein.

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=I54;

RA Jazayeri M., Sran N., Gish R., Basuni A.A., Cooksley G., Locarnini S.,

RA Carman W.F.;

RT "HBV core sequence: definition of genotype-specific variability and

RT correlation with geographic origin.,"

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF324140; AAL31853.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

SQ SEQUENCE 183 AA; 21100 MW; 62D9CA5700042559 CRC64;

Query Match 98.1%; Score 953; DB 12; Length 183;

Best Local Similarity 98.4%; Pred. No. 2.2e-89;

Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

QY 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLLWFHISCLTFFGTETVIEYL 120

DB 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLLWFHISCLTFFGTETVIEYL 120

QY 121 SGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

DB 121 SGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

QY 181 SOC 183

DB 181 SOC 183

RESULT 3

Q89437

ID Q89437 PRELIMINARY; PRT; 183 AA.

AC Q89437:

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)

DE Core protein (X, PREC and C genes) (CASTAA 2).

GN CORE.

OS Hepatitis B virus, and

OS Hepatitis B virus (subtype ayw).

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10407, 10418;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus; STRAIN=I59;

RA Jazayeri M., Sran N., Gish R., Basuni A.A., Cooksley G., Locarnini S.,

RA Carman W.F.;

RT "HBV core sequence: definition of genotype-specific variability and

RT correlation with geographic origin.,"

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw);

RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw);

RA Karayiannis P.;

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=Hepatitis B virus (subtype ayw);

RA Karayiannis P.;

RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF324146; AAL31859.1; -

DR EMBL; X85289; CAA59607.1; -

DR EMBL; X80925; CAA56888.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1.

SQ SEQUENCE 183 AA; 21102 MW; 2BB902063F253228 CRC64;

Query Match 98.1%; Score 953; DB 12; Length 183;

Best Local Similarity 98.4%; Pred. No. 2.2e-89;

Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60



```

DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE HBCAG (PRE-CORE protein) (PRECORE/core protein).
OS Hepatitis B virus (subtype ayw), and
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10418, 10407;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-SUB-TYPE AYW;
RX MEDLINE=94079539; PubMed=8257295;
RA Preisler-Adams S., Schlager M.J., Peters T., Hettler F., Gerok W.,
RA Pasenack J.,
RT "sequence analysis of hepatitis B virus DNA in immunologically
RT negative infection.";
RL Arch. Virol. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-AYW;
RA Karayiannis P.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus (subtype ayw); STRAIN-AYW;
RA Karayiannis P.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus; STRAIN=I43-Fam G;
RA Zampino R., Lobello S., Chiaramonte M., Venturi-Pasini C., Dumpis U.,
RA Thurez M., Karayiannis P.;
RT "Intra-familial transmission of Hepatitis B virus in Italy:
RT Phylogenetic sequence analysis and amino acid variation of the core
RT gene.";
RL J. Hepatol. 0:0-0(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-Hepatitis B virus; STRAIN=Gam1119F29, and Gam1821P217;
RA Dumpis U., Mendy M., Karayiannis P.;
RT "Prevalence of HBV core promoter/precore/core mutations in Gambian
RT chronic carriers.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; X72702; CAA51257.1; -
DR EMBL; X80925; CAA56887.1; -
DR EMBL; AF419525; AAL15953.1; -
DR EMBL; AF350127; AAK57244.1; -
DR EMBL; AF350205; AAK57322.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1
DT CHAIN 30 212
RP SEQUENCE 212 AA; 24336 MW; 1861B13E8B047AC8 CRC64;
Query Match 98.1%; Score 953; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.7e-89;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 SQC 212
RESULT 8
Query Match 98.1%; Score 953; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.7e-89;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 SQC 212

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O11884
ID O11884 PRELIMINARY; PRT; 212 AA.
AC O11884;
DT 01-JUL-1997 (TREMELrel. 04, Created)
DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Core antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Rao B.S., Casey J.L., Rinaudo J.S., Korba B.E.;
RT "Complete nucleotide sequence of a molecular clone of hepatitis B
RT virus from the 2.2.15 cell line.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U95551; AAB59971.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24360 MW; D301689E8B05A1B8 CRC64;
Query Match 97.9%; Score 951; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.3e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120
DB 90 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 180
DB 150 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTPSPRRRSQSPRRRSQSRE 209
QY 181 SQC 183
DB 210 PQC 212
RESULT 9
Q68025
ID Q68025 PRELIMINARY; PRT; 212 AA.
AC Q68025;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Pre-c/core protein.
GN PRE-C/CORE.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85293; CAA59616.1; -
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; 6940D04E90A410C3 CRC64;
Query Match 97.9%; Score 951; DB 12; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.3e-89;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

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Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149  
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
QY 181 SQC 183  
Db 210 SQC 212

## RESULT 10

Q68068 PRELIMINARY; PRT; 212 AA.  
AC Q68068;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Pre-c/core protein.  
OS Hepatitis B virus.  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: X85315; CAA59664.1; -  
DR InterPro: IPR002006; Hepatitis\_core.  
DR Pfam: PF00906; Hepatitis\_core; 1.  
SQ SEQUENCE 212 AA; 24366 MW; CEABDD4E8B11E5E8 CRC64;

Query Match 97.9%; Score 951; DB 12; Length 212;  
Best Local Similarity 98.4%; Pred. No. 4.3e-89;  
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 89  
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120  
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149  
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
QY 181 SQC 183  
Db 210 SQC 212

## RESULT 11

Q68070 PRELIMINARY; PRT; 212 AA.  
AC Q68070;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Pre-c/core protein.  
OS Hepatitis B virus.  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: X85316; CAA59666.1; -  
DR InterPro: IPR002006; Hepatitis\_core.  
DR Pfam: PF00906; Hepatitis\_core; 1.  
SQ SEQUENCE 212 AA; 24376 MW; D30173662996A1B8 CRC64;

Query Match 97.8%; Score 950; DB 12; Length 212;  
Best Local Similarity 98.4%; Pred. No. 5.4e-89;  
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 89  
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120  
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149  
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
QY 181 SQC 183  
Db 210 SQC 212

## RESULT 12

Q67984 PRELIMINARY; PRT; 212 AA.  
AC Q67984;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Pre-c/core protein.  
GN PRE-C/CORE.  
OS Hepatitis B virus.  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: X85256; CAA59519.1; -  
DR InterPro: IPR002006; Hepatitis\_core.  
DR Pfam: PF00906; Hepatitis\_core; 1.  
SQ SEQUENCE 212 AA; 24322 MW; 629E0B298B13D0D1 CRC64;

Query Match 97.8%; Score 950; DB 12; Length 212;  
Best Local Similarity 98.4%; Pred. No. 5.4e-89;  
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVELLSFLPSDFPVSVDLLDTASALYREALSPHCHSPHHTALRQAIL 89  
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 120  
Db 90 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWFHISCLTFGRETVEIYLV 149  
QY 121 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 150 SFGVWIRTPPAYPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
QY 181 SQC 183  
Db 210 SQC 212

## RESULT 13

Q68032 PRELIMINARY; PRT; 212 AA.  
AC Q68032;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Pre-c/core protein.  
GN PRE-C/CORE.

OS Hepatitis B virus.  
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA Lai M.E., Mazzoleni A.P., Porru A., Balestrieri A.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

DR EMBL; X85296; CAA59622.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1

SQ SEQUENCE 212 AA; 24308 MW; E28972C78B1604FF CRC64;

Query Match

Best Local Similarity 97.8%; Score 950; DB 12; Length 212;

Matches 179; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

RESULT 14

QY1SV7

ID QY1SV7 PRELIMINARY; PRT; 212 AA.

AC QY1SV7;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA Dumpis U., Mendy M., Karayiannis P.;

RL "Prevalence of HBV core promoter/precure/core mutations in Gambian

chronic carriers";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF350155; AAK57272.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1

SQ SEQUENCE 212 AA; 24363 MW; 27E96F6D069BC35A CRC64;

Query Match

Best Local Similarity 97.8%; Score 948; DB 12; Length 212;

Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

Db 210 SOC 212

RESULT 15

QY1SZ5

ID QY1SZ5 PRELIMINARY; PRT; 212 AA.

AC QY1SZ5;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Precore/core protein.

OS Hepatitis B virus.

OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA Dumpis U., Mendy M., Karayiannis P.;

RL "Prevalence of HBV core promoter/precure/core mutations in Gambian

chronic carriers";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF350134; AAK57251.1; -

DR InterPro: IPR002006; Hepatitis\_core.

DR Pfam: PF00906; Hepatitis\_core; 1

SQ SEQUENCE 212 AA; 24363 MW; 9EF3ADC58CF9CB78 CRC64;

Query Match

Best Local Similarity 97.6%; Score 948; DB 12; Length 212;

Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60

DB 30 MDIDPYKEGATVALLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 89

QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

DB 90 CWGELMTLATWGVNLEDPASDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 180

DB 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSRPRRTSPRRRSQSRRRSQSRE 209

QY 181 SOC 183

DB 210 SOC 212

Search completed: August 6, 2003, 09:45:57

Job time : 96 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:31:33 ; Search time 24 Seconds  
(without alignments)  
358.579 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEGATVLLSFLP.....RRRSQSPRRRSQSRQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	956	98.5	183	1	CORA_HPBVY
2	937	96.5	183	1	CORA_HPBVZ
3	932	96.0	211	1	CORA_HPBVA
4	924	95.2	183	1	CORA_HPBVJ
5	924	95.2	183	1	CORA_HPBVO
6	924	95.2	185	1	CORA_HPBVM
7	923	95.1	183	1	CORA_HPBV4
8	916	94.3	185	1	CORA_HPBV2
9	908	93.5	214	1	CORA_HPBV9
10	906	93.3	195	1	CORA_HPBVF
11	904	93.1	183	1	CORA_HPBVL
12	901	92.8	212	1	CORA_HPBVT
13	672.5	69.3	188	1	CORA_HBV1
14	671	69.1	217	1	CORA_HPBGS
15	664	68.4	187	1	CORA_HBVH8
16	173	17.8	305	1	CORA_HPBHE
17	154.5	15.9	305	1	CORA_HPBDC
18	152.5	15.7	305	1	CORA_HPBDB
19	151	15.6	305	1	CORA_HPBWD
20	149.5	15.4	305	1	CORA_HPBDO
21	97	10.0	196	1	SFR2_CAEEL
22	94.5	9.7	219	1	NOL3_HUMAN
23	90.5	9.3	208	1	YSX2_CAEEL
24	90.5	9.3	1007	1	PR4B_HUMAN
25	90.5	9.3	1007	1	PR4E_MOUSE
26	88	9.1	253	1	GHX2_RAT
27	87.5	9.0	484	1	SFRB_HUMAN
28	87	9.0	3148	1	HD_FUGRU
29	83.5	8.6	1195	1	KCH7_MOUSE
30	83	8.5	253	1	GHX2_MOUSE
31	83	8.5	306	1	RM45_MOUSE
32	80.5	8.3	955	1	T150_HUMAN
33	80.5	8.3	1195	1	KCH7_RAT

34 78.5 8.1 483 1 VE2\_HPV14  
35 78 8.0 503 1 VE2\_HPV21  
36 77.5 8.0 498 1 VE2\_HPV08  
37 77.5 8.0 3695 1 LMA5\_HUMAN  
38 77 7.9 576 1 CATA\_RHOCA  
39 76 7.8 164 1 SFR3\_HUMAN  
40 76 7.8 540 1 HXTD\_YEAST  
41 76 7.8 784 1 DPO2\_AERPE  
42 75.5 7.8 557 1 MK04\_HUMAN  
43 75.5 7.8 1048 1 SRA4\_RAT  
44 75.5 7.8 1874 1 POLR\_KYMWJ  
45 75 7.7 331 1 YOO1\_CAEEL

P36783 human papill  
P50767 human papill  
P06422 human papill  
O15230 homo sapien  
P37743 rhodobacter  
P23152 homo sapien  
P42833 saccharomyc  
O93746 aeropyrum p  
P31152 homo sapien  
O63627 rattus norv  
P36304 kennedya ye  
P34633 caenorhabdi

## ALIGNMENTS

RESULT 1  
CORA\_HPBVY ID CORA\_HPBVY STANDARD; PRT; 183 AA.  
AC P03146;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype ayw).  
OC Viruses; Retrovird viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10418;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012091; PubMed=399327;  
RA Galibert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;  
RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)  
cloned in E. coli.";  
RL Nature 281:646-650(1979).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Latvia;  
RX MEDLINE=85204397; PubMed=3996597;  
RA Bichko V., Pushko P., Dreilina D., Pumpen P., Gren E.;  
RT "Subtype ayw variant of hepatitis B virus. DNA primary structure  
analysis.";  
RL FEBS Lett. 185:208-212(1985).  
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or send an email to license@isb-sib.ch).  
DR EMBL; V01460; CAA24706.1; ALT\_INIT.  
DR EMBL; X02496; -; NOT\_ANNOTATED\_CDS.  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 162 169  
FT REPEAT 170 177  
FT VARIANT 33 33 T -> N (IN STRAIN LATVIA).  
FT VARIANT 80 80 A -> I (IN STRAIN LATVIA).  
SQ SEQUENCE 183 AA; 21116 MW; E0D9D9763F24E958 CRC64;  
Query Match 98.5%; Score 956; DB 1; Length 183;  
Best Local Similarity 98.9%; Pred. No. 2.3e-80;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVLLSFLPSPDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60  
DB 1 MDIDPYKEGATVLLSFLPSPDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60  
QY 61 CWGELMTATWGVNLDPASRLVSVYNTNMGKFRQLLWFLHISCLTFGTETVIELV 120

Db 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120  
QY 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 180  
Db 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 180  
QY 181 SOC 183  
Db 181 SOC 183

## RESULT 2

ID CORA\_HPBVZ STANDARD; PRT; 183 AA.  
AC P03147;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-1989 (Rel. 12, Last annotation update)  
DE Core antigen.  
GN C.

OS Hepatitis B virus (subtype ady).  
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10419;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81012115; PubMed=399329;

RA Pasek M., Goto T., Gilbert W., Zink B., Schaller H., McKay P.,

RA Leadbetter G., Murray K., and their expression in E. coli.";

RT "Hepatitis B virus genes and their expression in E. coli.";

RL Nature 282:575-579(1979).

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EMBL: J02202; AAA45486.1; -

EMBL: A08967; CAA00816.1; -

PIR: B93217; NKVLAL2.

InterPro: IPR002006; Hepatitis\_core.

Pfam: PF00906; Hepatitis\_core; 1.

Core protein; Repeat.

REPEAT 162 169

FT REPEAT 170 177

SEQUENCE 183 AA; 21042 MW; 545ED0E5527F26C CRC64;

Query Match 96.5%; Score 937; DB 1; Length 183;

Best Local Similarity 95.6%; Pred. No. 1.3e-78;

Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTAAALYRDALESPEHCSPHHTALRQAIL 60

QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120

Db 61 CWGDLMTLATVGTNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120

QY 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 180

Db 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 180

QY 181 SOC 183

Db 181 SOC 183

## RESULT 3

CORA\_HPBVA

ID CORA\_HPBVA STANDARD; PRT; 211 AA.  
AC P24023;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Core antigen.  
GN C.

OS Hepatitis B virus (strain alpha).

OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.

OX NCBI\_TaxID=10411;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90266476; PubMed=2345966;

RA Tong S., Li J., Vitvitski L., Trepo C.;

RT "Active hepatitis B virus replication in the presence of anti-HBe is

associated with viral variants containing an inactive pre-C region.";

RL Virology 176:596-603(1990).

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EMBL: M32138; -; NOT\_ANNOTATED\_CDS.

PIR: A34773; NKVLAL.

InterPro: IPR002006; Hepatitis\_core.

Pfam: PF00906; Hepatitis\_core; 1.

Core protein; Repeat.

REPEAT 183 190

FT REPEAT 198 206

SEQUENCE 211 AA; 24208 MW; B774AC72E65C75AB CRC64;

Query Match 96.0%; Score 932; DB 1; Length 211;

Best Local Similarity 95.6%; Pred. No. 4.3e-78;

Matches 175; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60

Db 29 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 88

QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 120

Db 89 CWGDLTLSTWVGNGLEDPTSRDLVSVYVNTNMGLKFRQLLWFHISCLTFFGRETVEYLV 148

QY 121 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 180

Db 149 SFGVWIRTPPAYRPNAPILSTLPTETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 208

QY 181 SOC 183

Db 209 SOC 211

## RESULT 4

ID CORA\_HPBVJ STANDARD; PRT; 183 AA.  
AC P17391;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Core antigen.  
OS Hepatitis B virus (subtype adw / strain Japan/pJDW233).  
OC Viruses; Retrovirus; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10413;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89010694; PubMed=3171552;

RA Okamoto H., Tsuda F., Sakugawa H., Sastrosoewignjo R.I., Imai M.,

RA Miyakawa Y., Mayumi M.;

RT "Typing hepatitis B virus by homology in nucleotide sequence:



Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSRRRSQS 180  
QY 179 RESQC 183  
Db 181 RESQC 185

## RESULT 7

CORA\_HPBV4  
ID CORA\_HPBV4 STANDARD; PRT; 183 AA.  
AC P03150; P03151;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype adr4),  
OS Hepatitis B virus (subtype adr), and  
OS Hepatitis B virus (subtype adr) / strain Indonesia/PIDW420).  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10409, 106820, 10412;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ADR;  
RX MEDLINE=83168919; PubMed=6300776;  
RA Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;  
RT "The complete nucleotide sequences of the cloned hepatitis B virus  
DNA; subtype adr and adr.";  
RL Nucleic Acids Res. 11:1747-1757(1983).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ADR4;  
RX MEDLINE=83246570; PubMed=6306594;  
RA Fujiyama A., Miyahara A., Nozaki C., Yoneyama T., Ohtomo N.,  
RA Matsubara K.;  
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype  
adr.";  
RL Nucleic Acids Res. 11:4601-4610(1983).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ADR;  
RX MEDLINE=89010694; PubMed=3171552;  
RA Okamoto H., Tsuda F., Sakugawa H., Sastrosowigno R.I., Imai M.,  
RA Miyakawa Y., Mayumi M.;  
RT "Typing hepatitis B virus by homology in nucleotide sequence:  
comparison of surface antigen subtypes.";  
RL J. Gen. Virol. 69:2575-2583(1988).

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-----  
DR EMBL; V00867; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; X01587; CAA25745.1; -;  
DR EMBL; D00331; -; NOT\_ANNOTATED\_CDS.  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 162 169  
FT REPEAT 170 177  
SQ SEQUENCE 183 AA; 21095 MW; ED2DA1DB07FB596D CRC64;

Query Match 95.1%; Score 923; DB 1; Length 183;  
Best Local Similarity 94.5%; Pred. No. 2.4e-77;  
Matches 173; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCHSPHHTALRQAIL 60  
|||||

Db 1 MDIDPYKEFGASVELLSFLPSDFPVSVDLDTASALYREALSPHCHSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLMFHSICLTFGRETVEYLV 120  
|||||  
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLMFHSICLTFGRETVEYLV 120  
|||||  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSRRRSQSRE 180  
|||||  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSRRRSQSRE 180  
|||||  
QY 181 SOC 183  
Db 181 SOC 183  
Db 181 SOC 183

## RESULT 8

CORA\_HPBV2  
ID CORA\_HPBV2 STANDARD; PRT; 185 AA.  
AC P03148;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype adr2).  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10408;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Valenzuela P., Quiroga M., Zaldívar J., Gray P., Rutter W.J.;  
RL (in) Field B.N., Jaenisch R., Fox C.F. (eds.);  
RL Animal virus genetics, pp.57-70, Academic Press, New York (1980).  
DR InterPro; IPR002006; Hepatitis\_core.  
DR Pfam; PF00906; Hepatitis\_core; 1.  
KW Core protein; Repeat.  
FT REPEAT 164 171  
FT REPEAT 172 179  
SQ SEQUENCE 185 AA; 21304 MW; 31F4DC338B507E19 CRC64;

Query Match 94.3%; Score 916; DB 1; Length 185;  
Best Local Similarity 94.6%; Pred. No. 1.1e-76;  
Matches 175; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCHSPHHTALRQAIL 60  
|||||  
Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCHSPHHTALRQAIL 60  
|||||  
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLMFHSICLTFGRETVEYLV 120  
|||||  
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLMFHSICLTFGRETVEYLV 120  
|||||  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRR--PGRSPRRRTSPRRRSQSRRRSQS 178  
|||||  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRDRGRSPRRRTSPRRRSQSRRRSQS 180  
|||||  
QY 179 RESQC 183  
Db 181 RESQC 185

## RESULT 9

CORA\_HPBV9  
ID CORA\_HPBV9 STANDARD; PRT; 214 AA.  
AC P17099;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Core antigen.  
GN C.  
OS Hepatitis B virus (subtype adr / strain 991).  
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10410;  
RN [1]

```

RP SEQUENCE FROM N.A.
RA Koechel H.G., Schueler A., Lottmann S., Thomssen R.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
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DR EMBL; X51970; CAA36232.1; -
DR PIR; S10381; NKVLKS.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 2D668333EC5AFB8C CRC64;

Query Match 93.5%; Score 908; DB 1; Length 214;
Best Local Similarity 94.6%; Pred. No. 6.7e-76;
Matches 175; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 30 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 89
QY 61 CWGELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYL 120
DB 90 CWGELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYL 149
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 178
DB 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 209
QY 179 RESQC 183
DB 210 RESQC 214

RESULT 10
CORA_HPBVF STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (subtype adw2 variant sf).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169850; PubMed=2307406;
RA Bhat R.A., Ulrich P.P., Vyas G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man.";
RL Hepatology 11:271-276(1990).
DR PIR; A37182; NKVLH3.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 174 181
FT REPEAT 182 189
SQ SEQUENCE 195 AA; 22461 MW; E2B166F879CB7CB7 CRC64;

Query Match 93.3%; Score 906; DB 1; Length 195;
Best Local Similarity 93.4%; Pred. No. 9.2e-76;
Matches 171; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 13 LDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYRESLESDDHCSPHHTALRQAIL 72
QY 61 CWGELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYL 120
DB 73 CWELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYL 132
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 180
DB 133 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 192
QY 181 SQC 183
DB 193 SQC 195

RESULT 11
CORA_HPBVL STANDARD; PRT; 183 AA.
AC P12901;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Core antigen.
GN C.
OS Hepatitis B virus (strain lsh / chimpanzee isolate).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10414;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258473; PubMed=2838576;
RA Vaudin M., Wolstenholme A.J., Tsiquaye K.N., Zuckerman A.J.,
RA Harrison I.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee.";
RL J. Gen. Virol. 69:1383-1389(1988).
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DR EMBL; D00220; BAA00157.1; -
DR PIR; A28885; NKVLCP.
DR PDB; 1HHH; 31-OCT-93.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat; 3D-structure.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20959 MW; 923DCB94A33FC0E8 CRC64;

Query Match 93.1%; Score 904; DB 1; Length 183;
Best Local Similarity 93.4%; Pred. No. 1.3e-75;
Matches 171; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
DB 1 MDIDPYKEFGATVELLSPLSPDFPSVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
QY 61 CWGELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKFRQLLWFHISCLTFCGTETVIEYL 120
DB 61 CWGELMTLATWVGNNLEDPASRDVLVSVYVNTNMGLKIRQLLWFHISCLTFCGTETVIEYL 120
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 180
DB 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQ 180
QY 181 SQC 183

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Db 181 SOC 183
RESULT 12
COR_A_HPBVT STANDARD; PRT; 212 AA.
AC Q05495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Core antigen.
GN Hepatitis B virus (subtypes adw4 / strain Brazil / isolate w4B).
OS Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=45410;
OX [1]
RN SEQUENCE FROM N.A.
RP SPECIES=Woodchuck hepatitis virus 1;
RX MEDLINE=93346970; PubMed=8345335;
RA Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R.,
RA Gerlich W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4.";
RL J. Gen. Virol. 74:1627-1632(1993).
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DR EMBL; X69798; CAA49452.1; -
DR PIR; JQ2227; JQ2227.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT DOMAIN 178 204 ARG-RICH.
FT DOMAIN 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
FT REPEAT 184 198 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
SQ SEQUENCE 212 AA; 24234 MW; F832610DB7C36FD2 CRC64;

Query Match 92.8%; Score 901; DB 1; Length 212;
Best Local Similarity 92.3%; Pred. No. 2.9e-75;
Matches 169; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

1 MDIDPYKEGATVVELLSFLPSDFPVSRLDLDTSALYREALSPHCHTALRQAIL 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
30 MDIDPYKEGASVELLSFLPSDFPVSRLDLDTSALYREALSPHCHTALRQAIL 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 CWGELMTLATVYGVNLEDPASRDLYVYVNTNMGKLFROLLWFHISCLTFGTVEYLV 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 CWGELMTLASVYGVNLEDPASRDLYVYVNTNMGKLFROLLWFHISCLTFGTVEYLV 149
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 SFGVWIRTPPAYRPPNAPILSTLPETTVYVRPGSPRRRPSQSPRRR 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
150 SFGVWIRTPPAYRPPNAPILSTLPETTVYVRPGSPRRRPSQSPRRR 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 SOC 183
210 SOC 212
Db 181 SOC 183
RESULT 13
COR_A_HWB1 STANDARD; PRT; 188 AA.
AC F03152;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Core antigen.
GN Woodchuck hepatitis virus 1 (WHV 1);
OS Woodchuck hepatitis virus 7 (WHV 7);
OS Woodchuck hepatitis virus 59 (WHV 59), and
OS Woodchuck hepatitis virus 8 (infectious clone) (WHV 8).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10430, 10432, 10431, 10434;
RN [1]
RN SEQUENCE FROM N.A.
RP SPECIES=Woodchuck hepatitis virus 1;
RX MEDLINE=82216969; PubMed=7086958;
RA Galibert F., Chen T.N., Mandart E.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. Virol. 41:51-65(1982).
RN [2]
RN SEQUENCE FROM N.A.
RP SPECIES=Woodchuck hepatitis virus 7, and Woodchuck hepatitis virus 59;
RX MEDLINE=88101359; PubMed=3336938;
RA Cohen J.I., Miller R.H., Rosenblum B., Denniston K., Gerin J.L.,
RA Purcell R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";
RL Virology 162:12-20(1988).
RN [3]
RN SEQUENCE FROM N.A.
RP SPECIES=Woodchuck hepatitis virus 8 (infectious clone);
RX MEDLINE=89184524; PubMed=2928306;
RA Girones R., Cote P.J., Hornbuckle W.E., Tennant B.C., Gerin J.L.,
RA Purcell R.H., Miller R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1846-1849(1989).
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DR EMBL; J02442; AAA46761.1; -
DR EMBL; M18752; AAA46769.1; -
DR EMBL; M19183; AAA46765.1; -
DR EMBL; J04514; AAA46772.1; -
DR PIR; C32397; NKVLC.
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
KW Core protein; Repeat.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; 1F4454D0A7B7CE42 CRC64;

Query Match 69.3%; Score 672.5; DB 1; Length 188;
Best Local Similarity 66.5%; Pred. No. 1.8e-54;
Matches 125; Conservative 20; Mismatches 38; Indels 5; Gaps 1;

1 MDIDPYKEGATVVELLSFLPSDFPVSRLDLDTSALYREALSPHCHTALRQAIL 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MDIDPYKEGSSYQLNLFPLDFPDNALVDATYALYEEETGTHCHSPHCHTALRQALV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 CWGELMTLATVYGVNLEDPASRDLYVYVNTNMGKLFROLLWFHISCLTFGTVEYLV 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 CWDELTKLIAMSSNITSEOVETIIVNVNDTWGLKVRQSLWFLHISCLTFGTVEYLV 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 SFGVWIRTPPAYRPPNAPILSTLPETTVYVRPGSPRRRPSQSPRRR 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 SFGVWIRTPPAYRPPNAPILSTLPETTVYVRPGSPRRRPSQSPRRR 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 SOSRESQC 183
||| :
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[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=86062931; PubMed=3855246;
RX      Kodama K., Ogasawara N., Yoshikawa H., Murakami S.;
RA      "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT      evolutionary relationship between hepadnaviruses.";
RL      J. Virol. 56:978-986(1985).
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CC      ENML; M11082; AAA19185.1; -.
DR      PIR; A03714; NKVLC2.
DR      InterPro; IPR002006; Hepatitis_core.
DR      Pfam; PF00906; Hepatitis_core; 1.
KW      Core protein; Repeat.
FT      REPEAT   166 173
FT      REPEAT   174 181
SQ      SEQUENCE   187 AA;  21579 MW;  D4BC446FF7163165 CRC64;

Query Match          68.4%; Score 664; DB 1; Length 187;
Best Local Similarity 56.3%; Pred. No. 1.le-53;
Matches 124; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

Qy      1 MDIDPYKEFGATVELLSFLPSDFSPVRDLDTASALYREALSEPHCSPHHTALRQAIL 60
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MDIDPYKEFGSSQLNLFLPDDFPDUNALVDATALYEELTGREHCSPHHTAIRQAIV 60
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      61 CWGELMTLATWVGVLNDELDPASRDLYSYVNNTMGLKFRQLLWFHISCLTFGTETVIEYL 120
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 CWDELTKLIAWMSNITSEQVRTIIVNHVNDTWGLKVRSQLWFLHSCLTFGQHTVOEFLV 120
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      121 SFGWVIRTTPAYPPNPAPILSTLPETVVRRPG----RSPRRRTPSPPRRRSOSPPRRRS 176
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      121 SFVWVIRTTPAYPPNPAPILSTLPETVTVIRRGARARSPPRRTPSPRRRSOSPPRRRS 180
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      177 QSRSEQC 183
         || : |
Db      181 QSPSANC 187
```

Search completed: August 6, 2003, 09:44:15  
Job time : 26 secs

```

Db          181 SQSPSANC 188

RESULT 14
CORA_HPBGS
ID          STANDARD;          PRT;    217 AA.
AC          P03153;
DT          21-JUL-1986 (Rel. 01, Created)
DT          21-JUL-1986 (Rel. 01, Last sequence update)
DT          01-JAN-1990 (Rel. 13, Last annotation update)
DE          Core antigen.
DE          C.
GN          C.
OS          Ground squirrel hepatitis virus (GSHV).
OC          Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX          NCBI_TaxID=10406;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=84267998; PubMed=6086950;
RA          Seeger C., Ganem D., Varmus H.E.;
RT          "Nucleotide sequence of an infectious molecularly cloned genome of
RL          ground squirrel hepatitis virus.";
RR          J. Virol. 51:367-375(1984).
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
CC          modified and this statement is not removed. Usage by and for commercial
CC          entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC          or send an email to license@isb-sib.ch).
CC          -----
CC          EMBL; K02715; AAA6755.1; -.
CC          PIR; A03715; NKVLS.
CC          InterPro; IPR002006; Hepatitis_core.
CC          Pfam; PF00906; Hepatitis_core; 1.
CC          Core protein; Repeat.
CC          REPEAT 196
CC          REPEAT 204 211
CC          SEQUENCE 217 AA; 225189 MW; DF489467355EC11A CRC64;
SQ

```

Query Match	69.1%	Score	671;	DB 1;	Length	217;			
Best Local Similarity	67.6%	Pred. No.	2.9e-54;						
Matches	127;	Conservative	18;	Mismatches	37;	Indels	6;	Gaps	2;
QY	1	MDIDPKYKFGATWELLSFLPSDFPSSVRDLDTAFASLYREALSPEHCSPHHATRAQAIL	60						
Db	31	MDIDPKYKFGSSVQLNLFPLDFPDLNALVDYFAALYEELTGRCHCSPHHATRAQALV	90						
QY	61	CWGELMTLATWGVNLEDPASRDLVVSYYNTNMGKLFQRLQLWPHISCLTGETTVEYLV	120						
Db	91	CWEELTRLITWSENTEVEYRR-IIVDHVNNTWGLKVRQTLWFHLSCLTQGTWQBEFLV	149						
QY	121	SFGVWLRTPAYRPPNAPILSTLPEHTVTVRRPG-----SPPRRTSPSPRRSSQSPRRR	175						
Db	150	SFGVWLRTPAYRPPNAPILSTLPEHTVTVRRGGSRAARSPRRTSPSPRRSSQSPRRR	209						
QY	176	SQSRESQC	183						
Db	210	SOSPASNC	217						

RESULT 15	
CORA_WHV8	
ID	CORA_WHV8
STANDARD;	187 AA.
AC	P06433;
DT	01-JAN-1988 (Rel. 06, Created)
DT	01-JAN-1988 (Rel. 06, Last sequence update)
DT	01-OCT-1989 (Rel. 12, Last annotation update)
DE	Core antigen.
C.	
GN	Woodchuck hepatitis virus 8 (WHV 8).
OS	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC	NCBI_TaxID=10433;
OX	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:41:04 ; Search time 40 Seconds  
(without alignments)  
439.972 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPYKEGATVLLSLP.....RRRSQSPRRRRSQSRESQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	98.5	212	1	NKVLAH
2	953	98.1	212	2	S53211
3	953	98.1	212	2	S32204
4	953	98.1	212	2	S20750
5	951	97.9	212	2	S53216
6	951	97.9	212	2	S53272
7	950	97.8	212	2	S53225
8	950	97.8	212	2	S53274
9	950	97.8	212	2	S53163
10	947	97.5	183	2	S53247
11	947	97.5	183	2	S53270
12	947	97.5	212	2	S53251
13	947	97.5	212	2	S20746
14	946	97.4	183	2	S53169
15	946	97.4	212	2	S53159
16	946	97.4	212	2	S53200
17	946	97.4	212	2	S53202
18	945	97.3	212	2	S53281
19	945	97.3	212	2	S53198
20	944	97.2	212	2	S53223
21	944	97.2	212	2	S53227
22	941	96.9	212	2	S53253
23	941	96.9	212	2	S53204
24	939	96.7	183	2	S53260
25	939	96.7	212	1	NKVLH
26	938	96.6	212	2	S53240
27	937	96.5	183	1	NKVLH
28	937	96.5	183	2	S53181
29	936	96.4	212	2	S53242

#### ALIGNMENTS

##### RESULT 1

NKVLAH

e antigen precursor / core antigen - hepatitis B virus (subtype ayw4, isolate hb321 a)  
N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen  
N:Contains: core antigen; e antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: subtype ayw4, isolate hb321; isolate patient Ferracuti'83; isolate patient Cheri'83

C:Date: 18-Dec-1981 #sequence\_revision 08-Nov-1996 #text\_change 16-Jul-1999  
C:Accession: S47405; S53191; S53209; S53234; S53264; S53249; S53262; S53277; A03711  
R:Plucieniczak, A.  
submitted to the EMBL Data Library, August 1994

A:Description: Molecular cloning and sequencing of two complete genomes of polish iso  
A:Reference number: S47404  
A:Accession: S47405  
A:Molecule type: DNA

A:Residues: 1-212 <PLU>  
A:Cross-references: EMBL:Z35716; NID:q527435; PIDN:CAA84786.1; PID:q527437  
A:Experimental source: subtype ayw4, isolate hb321

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112

A:Accession: S53191  
A:Molecule type: DNA  
A:Residues: 1-212 <LA1>

A:Cross-references: EMBL:X85283; NID:q736088; PIDN:CAA59593.1; PID:q736090  
A:Experimental source: isolate patient Ferracuti'83  
A:Accession: S53209

A:Molecule type: DNA  
A:Residues: 1-212 <LA2>  
A:Cross-references: EMBL:X85290; NID:q736114; PIDN:CAA59609.1; PID:q736116

A:Experimental source: isolate patient Castag'83  
A:Accession: S53234  
A:Molecule type: DNA

A:Residues: 1-212 <LA3>  
A:Cross-references: EMBL:X85300; NID:q736150; PIDN:CAA59631.1; PID:q736152  
A:Experimental source: isolate patient Sanna'84

A:Accession: S53264  
A:Molecule type: DNA  
A:Residues: 1-212 <LA4>

A:Cross-references: EMBL:X85313; NID:q736194; PIDN:CAA59659.1; PID:q736196  
A:Experimental source: isolate patient Licheri'85  
A:Accession: S53249

A:Molecule type: DNA  
A:Residues: 1-212 <LA5>  
A:Cross-references: EMBL:X85306; NID:q736172; PIDN:CAA59644.1; PID:q736174

A:Experimental source: isolate patient Fiore'1'86  
A:Accession: S53262  
A:Molecule type: DNA

A:Residues: 1-212 <LA6>  
A:Cross-references: EMBL:X85312; NID:q736191; PIDN:CAA59657.1; PID:q736193  
A:Experimental source: isolate patient Licheri'83

30	935	96.3	183	2	S53129	core antigen - hep
31	935	96.3	183	2	S53152	core antigen - hep
32	932	96.0	183	2	S53140	core antigen - hep
33	932	96.0	211	1	NKVLH	e antigen precursor
34	932	96.0	212	2	S53257	e antigen precursor
35	931	95.9	212	2	S53279	e antigen precursor
36	930	95.8	212	2	S53229	e antigen precursor
37	930	95.8	212	2	S25651	e antigen precursor
38	929	95.7	183	2	S53232	core antigen - hep
39	928	95.6	212	2	S53255	e antigen precursor
40	927	95.5	183	2	S53189	core antigen - hep
41	927	95.5	212	2	S53238	e antigen precursor
42	927	95.5	214	2	S01405	core antigen - hep
43	925	95.3	183	2	S53267	core antigen - hep
44	925	95.3	183	2	S53137	core antigen - hep
45	924	95.2	212	1	NKVLH	e antigen precursor

A:Accession: S53277  
 A:Molecule type: DNA  
 A:Residues: 30-212 <LAI>  
 A:Cross-references: EMBL:X85317; NID:g736211; PIDN:CAA59669.1; PID:g736214.  
 A:Experimental source: patient Giordo-2'86  
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
 R:Galibert, F.; Mandat, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.  
 Nature 281, 646-650, 1979  
 A:Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. coli.  
 A:Reference number: A93214; MUID:81012091; PMID:399327  
 A:Accession: A03711  
 A:Molecule type: DNA  
 A:Residues: 1-212 <GAL>  
 A:Cross-references: GB:J02203; NID:g329640; PIDN:AAA45489.1; PID:g329642  
 A:Experimental source: subtype ayw  
 C:Genetics:  
 A:Gene: C  
 C:Superfamily: hepatitis B virus core antigen  
 C:Keywords: alternative initiators; core protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-212/Product: core antigen #status predicted <CAG>  
 F:30-178/Product: e antigen #status predicted <EAG>  
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.5%; Score 956; DB 1; Length 212;  
 Best Local Similarity 98.9%; Pred. No. 1.3e-76;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 60
DB	30	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 89
QY	61	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 120
DB	90	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 149
QY	121	SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSQSRRRSQSRE 180
DB	150	SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSQSRRRSQSRE 209
QY	181	SQC 183
DB	210	SQC 212

RESULT 2  
 S53211  
 e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag-1'85 and  
 Alternate names: HBC antigen; HBe antigen precursor / HBC antigen; pre-C/C antigen  
 Contains: core antigen; e antigen  
 C:Species: hepatitis B virus, HBV  
 A:Variety: isolate patient Castag-1'85; isolate patient Ferracuti-1'89  
 C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C:Accession: S53211; S53197  
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S53112  
 A:Accession: S53211  
 A:Molecule type: DNA  
 A:Residues: 1-212 <LAI>  
 A:Cross-references: EMBL:X85291; NID:g736117; PIDN:CAA59611.1; PID:g736119  
 A:Experimental source: isolate patient Castag-1'85  
 A:Accession: S53197  
 A:Molecule type: DNA  
 A:Residues: 30-212 <LAW>  
 A:Cross-references: EMBL:X85284; NID:g736095; PIDN:CAA59596.1; PID:g736098  
 A:Experimental source: isolate patient Ferracuti-1'89  
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C:Genetics:  
 A:Gene: C  
 C:Superfamily: hepatitis B virus core antigen  
 C:Keywords: alternative initiators; core protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>  
 F:30-178/Product: e antigen #status predicted <EAG>  
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 953; DB 2; Length 212;  
 Best Local Similarity 98.4%; Pred. No. 2.4e-76;  
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 60
DB	30	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 89
QY	61	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 120
DB	90	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 149
QY	121	SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSQSRRRSQSRE 180
DB	150	SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSQSRRRSQSRE 209
QY	181	SQC 183
DB	210	SQC 212

RESULT 3  
 S32204  
 e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patients C1000 a  
 Alternate names: HBe antigen precursor / HBC antigen; pre-C/C antigen  
 Contains: core antigen; e antigen  
 C:Species: hepatitis B virus, HBV  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Oct-2000  
 C:Accession: S32204; S53207  
 R:Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Rasenack, J.  
 submitted to the EMBL Data Library, March 1993  
 A:Description: Identification and sequence analysis of hepatitis B virus DNA in immun  
 A:Reference number: S32202  
 A:Accession: S32204  
 A:Molecule type: DNA  
 A:Residues: 1-212 <PR>  
 A:Cross-references: EMBL:X72702; NID:g288927; PIDN:CAA51257.1; PID:g288930  
 A:Experimental source: subtype ayw, patient C1000  
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S53112  
 A:Accession: S53207  
 A:Molecule type: DNA  
 A:Residues: 30-212 <LAI>  
 A:Cross-references: EMBL:X85289; NID:g736110; PIDN:CAA59607.1; PID:g736113  
 A:Experimental source: isolate patient Castag-2'87  
 A:Note: due to a stop codon mutation between the alternative initiators the e antigen  
 C:Genetics:  
 A:Gene: C  
 C:Superfamily: hepatitis B virus core antigen  
 C:Keywords: alternative initiators; core protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-212/Product: core antigen #status predicted <CAG>  
 F:30-178/Product: e antigen #status predicted <EAG>  
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 953; DB 2; Length 212;  
 Best Local Similarity 98.4%; Pred. No. 2.4e-76;  
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 60
DB	30	MDIDPYKEFGATVELLSFLPDSFVSRDLDTASALYREALSPHHTALRAAIL 89
QY	61	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 120
DB	90	CWGLMTLATWGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFTGTETVIELV 149
QY	121	SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSQSRRRSQSRE 180

```
|||||
Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Qy 181 SQC 183
Db 210 SQC 212

RESULT 4
S20750
e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient CI)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype ayw, patient CI
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S20750
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A:Reference number: S20745
A:Experimental source: subtype ayw, patient CI
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 953; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.4e-76;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 120
Db 90 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Db 150 AFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Qy 181 SQC 183
Db 210 SQC 212

RESULT 5
S53216
e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag'3)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Castag'3
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53216
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A:Reference number: S53112
A:Experimental source: isolate patient Castag'3
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 98.1%; Score 953; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 2.4e-76;
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 120
Db 90 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Db 150 AFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Qy 181 SQC 183
Db 210 SQC 212
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```
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.9%; Score 951; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.6e-76;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 120
Db 90 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 180
Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Qy 181 SQC 183
Db 210 SQC 212

RESULT 6
S53272
e antigen precursor / core antigen - hepatitis B virus (isolate patient Licheri-3'90)
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen
N:Contains: core antigen; e antigen
C:Species: hepatitis B virus, HBV
A:Variety: isolate patient Licheri-3'90
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 26-Aug-1999
C:Accession: S53272
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
Submitted to the EMBL Data Library, March 1995
Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negative
A:Reference number: S53112
A:Experimental source: isolate patient Licheri-3'90
C:Genetics:
A:Gene: C
C:Superfamily: hepatitis B virus core antigen
C:Keywords: alternative initiators; core protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-212/Product: core antigen #status predicted <CAG>
F:30-178/Product: e antigen #status predicted <EAG>
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.9%; Score 951; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.6e-76;
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 89
Qy 61 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 120
Db 90 CWGELMTLATWGVNLEDPASRDVWSYVNTNMGKFRQLLWFHISCLTFTGTETVIEYLV 149
Qy 121 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 180
Db 150 SFGVWIRTPPAYRPPNAPILLSTLPTTVVRRGRSPRRTPSPRRRSQSPPRRRSQSRE 209
Qy 181 SQC 183
```

Db 210 SOC 212

# RESULT 7

S53225  
e antigen precursor / core antigen - hepatitis B virus (isolate patient Chighine-2'86)  
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen  
N:Contains: core antigen; e antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Chighine-2'86  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53225  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53225  
A:Molecule type: DNA  
A:Residues: 1-212 <LAI>  
A:Cross-references: EMBL:X85296; NID:g736137; PIDN:CAA59622.1; PID:g736139  
A:Experimental source: isolate patient Chighine-2'86  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: alternative initiators; core protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-212/Product: core antigen #status predicted <CAG>  
F:30-178/Product: e antigen #status predicted <EAG>  
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.8%; Score 950; DB 2; Length 212;  
Best Local Similarity 97.8%; Pred. No. 4.4e-76;  
Matches 179; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 89  
QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 120  
Db 90 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 149  
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209  
QY 181 SOC 183  
Db 210 SOC 212

# RESULT 8

S53274  
e antigen precursor / core antigen - hepatitis B virus (isolate patient Giordo'84)  
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen  
N:Contains: core antigen; e antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Giordo'84  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53274  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53274  
A:Molecule type: DNA  
A:Residues: 1-212 <LAI>  
A:Cross-references: EMBL:X85316; NID:g736208; PIDN:CAA59666.1; PID:g736210  
A:Experimental source: isolate patient Giordo'84  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: alternative initiators; core protein  
F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>  
F:30-178/Product: e antigen #status predicted <EAG>  
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

# Query Match 97.8%; Score 950; DB 2; Length 212;

Best Local Similarity 98.4%; Pred. No. 4.4e-76;  
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 89  
QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 120  
Db 90 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 149  
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209  
QY 181 SOC 183  
Db 210 SOC 212

# RESULT 9

S53163  
e antigen precursor / core antigen - hepatitis B virus (isolate patient Vittorina'92)  
N:Alternate names: HBe antigen precursor / HBeC antigen; pre-C/C antigen  
N:Contains: core antigen; e antigen  
C:Species: hepatitis B virus, HBV  
A:Variety: isolate patient Vittorina'92  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: S53163  
R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S53112  
A:Accession: S53163  
A:Molecule type: DNA  
A:Residues: 1-212 <LAI>  
A:Cross-references: EMBL:X85256; NID:g736050; PIDN:CAA59519.1; PID:g736052  
A:Experimental source: isolate patient Vittorina'92  
C:Genetics:  
A:Gene: C  
C:Superfamily: hepatitis B virus core antigen  
C:Keywords: alternative initiators; core protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-212/Product: core antigen #status predicted <CAG>  
F:30-178/Product: e antigen #status predicted <EAG>  
F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

# Query Match 97.8%; Score 950; DB 2; Length 212;

Best Local Similarity 98.4%; Pred. No. 4.4e-76;  
Matches 180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 60  
Db 30 MDIDPYKEGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTALRQAIL 89  
QY 61 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 120  
Db 90 CWGELMTLATVGVNLEDPASRDVSVYVNTNMGLKFRQLLWFHISCLTFGTETVIELV 149  
QY 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 209  
QY 181 SOC 183  
Db 210 SOC 212

# RESULT 10

S53247  
 core antigen - hepatitis B virus (isolate patient Flore-2'91)  
 N:Alternate names: Hbc antigen  
 N:Contains: core antigen  
 C:Species: hepatitis B virus, HBV  
 A:Variety: isolate patient patient Flore-2'91  
 C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C:Accession: S53247  
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S53112  
 A:Accession: S53247  
 A:Molecule type: DNA  
 A:Residues: 1-183 <LAI>  
 A:Cross-references: EMBL:X85305; NID:g736168; PIDN:CAA59642.1; PID:g736171  
 A:Experimental source: Isolate patient patient Flore-2'91  
 A:Note: due to a stop codon between the alternative initiators the e antigen precursor  
 C:Genetics:  
 A:Gene: C  
 C:Superfamily: hepatitis B virus core antigen  
 C:Keywords: core protein

Query Match 97.5%; Score 947; DB 2; Length 183;  
 Best Local Similarity 97.8%; Pred. No. 6.9e-76;  
 Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120  
 Db 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180  
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180

Qy 181 SQC 183  
 Db 181 SQC 183

Query Match 97.5%; Score 947; DB 2; Length 183;  
 Best Local Similarity 97.8%; Pred. No. 6.9e-76;  
 Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120  
 Db 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180  
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180

Qy 181 SQC 183  
 Db 181 SQC 183

Query Match 97.5%; Score 947; DB 2; Length 183;  
 Best Local Similarity 97.3%; Pred. No. 6.9e-76;  
 Matches 178; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60  
 Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Qy 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120  
 Db 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180  
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180

Qy 181 SQC 183  
 Db 181 SQC 183

## RESULT 12

S53251

e antigen precursor / core antigen - hepatitis B virus (isolate patient Flore'85)  
 N:Alternate names: Hbc antigen precursor / Hbc antigen; pre-C/C antigen  
 N:Contains: core antigen; e antigen  
 C:Species: hepatitis B virus, HBV  
 A:Variety: isolate patient Flore'85  
 C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999  
 C:Accession: S53251  
 R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S53112  
 A:Accession: S53251  
 A:Molecule type: DNA  
 A:Residues: 1-212 <LAI>  
 A:Cross-references: EMBL:X85307; NID:g736175; PIDN:CAA59646.1; PID:g736177  
 A:Experimental source: Isolate patient Flore'85  
 C:Genetics:  
 A:Gene: C  
 C:Superfamily: hepatitis B virus core antigen  
 C:Keywords: alternative initiators; core protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-212/Product: core antigen #status predicted <CAG>  
 F:30-178/Product: e antigen #status predicted <EAG>  
 F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.5%; Score 947; DB 2; Length 212;

Best Local Similarity 97.8%; Pred. No. 8.1e-76;

Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

Db 30 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

Qy 61 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 120

Db 90 CWGELMTLATWVGYNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV 149

Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 180

Db 150 SFGVWIRTPPAYRPPNAPILSTLPTETTVRRPGSRPRRTSPRRRSQSPRRRSQSR 209

Qy 181 SQC 183

Db 210 SQC 212

## RESULT 13

S20746

e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient C)  
 N:Alternate names: Hbc antigen precursor / Hbc antigen; pre-C/C antigen  
 N:Contains: core antigen; e antigen  
 C:Species: hepatitis B virus, HBV  
 A:Variety: subtype ayw, patient C  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S20746  
 R:Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.  
 submitted to the EMBL Data Library, March 1992  
 A:Description: Sequence analysis of HBV genomes isolated from patients with HBsAg neg

A:Reference number: S20745

A:Accession: S20746

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X65257; NID:g59429; PIDN:CAA46350.1; PID:g59431

A:Experimental source: subtype ayw, patient C

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.5%; Score 947; DB 2; Length 212;

Best Local Similarity 97.8%; Pred. No. 8.1e-76;

Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

|||||

Db 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

|||||

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

|||||

Db 90 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

|||||

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

|||||

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

|||||

QY 181 SOC 183

|||||

Db 210 SOC 212

RESULT 14

S53169 core antigen - hepatitis B virus (isolate patient Muresu/89)

N:Alternate names: HBC antigen

N:Contains: core antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Muresu/89

C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53169

A:Residues: 1-183 <LAI>

A:Cross-references: EMBL:X85275; NID:g736057; PIDN:CAA59571.1; PID:g736060

A:Experimental source: isolate patient Muresu/89

A:Note: due to a stop codon between the alternative initiators the e antigen precursor

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

Query Match 97.4%; Score 946; DB 2; Length 183;

Best Local Similarity 97.3%; Pred. No. 8.4e-76;

Matches 178; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

|||||

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

|||||

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

|||||

Db 61 CWGELMTLATWGANLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

|||||

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

|||||

|||||

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRTPRRTPSPRRRSQSRRRSQSRE 180

QY 181 SOC 183

|||||

Db 181 SOC 183

RESULT 15

S53159

e antigen precursor / core antigen - hepatitis B virus (isolate patient Garrucciu/90)

N:Alternate names: HBe antigen precursor / HBe antigen; pre-C/C antigen

N:Contains: core antigen; e antigen

C:Species: hepatitis B virus, HBV

A:Variety: isolate patient Garrucciu/90

C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 26-Aug-1999

C:Accession: S53159

R:Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S53112

A:Accession: S53159

A:Molecule type: DNA

A:Residues: 1-212 <LAI>

A:Cross-references: EMBL:X85272; NID:g736044; PIDN:CAA59563.1; PID:g736046

A:Experimental source: isolate patient Garrucciu/90

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: alternative initiators; core protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-212/Product: core antigen #status predicted <CAG>

F:30-178/Product: e antigen #status predicted <EAG>

F:179-212/Domain: carboxyl-terminal propeptide #link EAG #status predicted <ECP>

Query Match 97.4%; Score 946; DB 2; Length 212;

Best Local Similarity 97.3%; Pred. No. 9.9e-76;

Matches 178; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 60

|||||

Db 30 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAIL 89

|||||

QY 61 CWGELMTLATWGVNLEDPASRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 120

|||||

Db 90 CWGELMTLATWGVNLEDPATRDLYVSYVNTNMGLKFRQLLWFHISCLTFGTETVIEYL 149

|||||

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 180

|||||

Db 150 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSRRRSQSRE 209

QY 181 SOC 183

|||||

Db 210 SOC 212

Search completed: August 6, 2003, 09:46:41

Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:46:04 ; Search time 50 Seconds  
(without alignments)  
434.661 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPKYKFGATVALLSFLP.....RRRRSQRRRRSQRRSQ 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	971	100.0	183	9	US-09-812-862-12
2	956	98.5	183	8	US-08-785-997-38
3	956	98.5	183	11	US-09-387-340-38
4	956	98.5	183	11	US-09-848-616-99
5	956	98.5	183	11	US-09-931-325A-170
6	956	98.5	183	11	US-09-386-591-38
7	956	98.5	183	15	US-10-243-739-39
8	956	98.5	183	15	US-10-244-065-39
9	956	98.5	212	10	US-09-929-955-11
10	956	98.5	212	14	US-10-104-966-11
11	954	98.2	183	11	US-09-848-616-102
12	954	98.2	183	15	US-10-243-739-42
13	954	98.2	183	15	US-10-244-065-42
14	953	98.1	183	11	US-09-848-616-104
15	953	98.1	183	11	US-09-848-616-105

Sequence 44, Appl  
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Sequence 45, Appl  
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Sequence 55, Appl  
Sequence 56, Appl  
Sequence 57, Appl  
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17 953 98.1 183 15 US-10-243-739-45  
18 953 98.1 183 15 US-10-244-065-44  
19 953 98.1 183 15 US-10-244-065-45  
20 953 98.1 212 11 US-09-848-616-107  
21 953 98.1 212 11 US-09-848-616-108  
22 953 98.1 212 11 US-09-848-616-109  
23 953 98.1 212 15 US-10-243-739-47  
24 953 98.1 212 15 US-10-243-739-48  
25 953 98.1 212 15 US-10-244-065-47  
26 953 98.1 212 15 US-10-244-065-48  
27 951 97.9 212 11 US-09-848-616-112  
28 951 97.9 212 11 US-09-848-616-113  
29 951 97.9 212 11 US-09-848-616-114  
30 951 97.9 212 15 US-10-243-739-52  
31 951 97.9 212 15 US-10-243-739-53  
32 951 97.9 212 15 US-10-243-739-54  
33 951 97.9 212 15 US-10-244-065-52  
34 951 97.9 212 15 US-10-244-065-53  
35 951 97.9 212 15 US-10-244-065-54  
36 950 97.8 212 11 US-09-848-616-115  
37 950 97.8 212 11 US-09-848-616-116  
38 950 97.8 212 11 US-09-848-616-117  
39 950 97.8 212 15 US-10-243-739-49  
40 950 97.8 212 15 US-10-243-739-55  
41 950 97.8 212 15 US-10-243-739-56  
42 950 97.8 212 15 US-10-243-739-57  
43 950 97.8 212 15 US-10-244-065-49  
44 950 97.8 212 15 US-10-244-065-55  
45 950 97.8 212 15 US-10-244-065-56

#### ALIGNMENTS

#### RESULT 1

US-09-812-862-12  
Sequence 12, Application US/09812862  
Patent No. US20020035081A1

#### GENERAL INFORMATION:

APPLICANT: Wands, Jack R.  
Scaglioni, Pier Paolo  
Melegari, Margherita  
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/812,862  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>

#### PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667,073  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/492,489  
FILING DATE: 20-JUN-1995

#### ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/282001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906

```
;
;
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-812-862-12

Query Match      100.0%; Score 971; DB 9; Length 183;
Best Local Similarity 100.0%; Pred. No. 5e-86;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFWHISCLTFFGTETVIEYL 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
DB 181 SOC 183

RESULT 2
US-08-785-997-38
; Sequence 38, Application US/08785997
; Publication No. US20030021804A1
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-785-997-38

Query Match      100.0%; Score 971; DB 9; Length 183;
Best Local Similarity 100.0%; Pred. No. 5e-86;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
QY 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFWHISCLTFFGTETVIEYL 120
DB 61 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLLWFWHISCLTFFGTETVIEYL 120
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
DB 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
QY 181 SOC 183
DB 181 SOC 183

RESULT 3
US-09-387-340-38
; Sequence 38, Application US/09387340
; Publication No. US20030026808A1
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,340
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-387-340-38

Query Match      98.5%; Score 956; DB 11; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
DB 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60
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Qy	61	CWGEMLTATWGVNLEDPASRDLYVSVYVNTMGLKFRQLLWFIISCLTFTGRTVTEYLV	120
Db	61	CWGEMLTATWGVNLEDPASRDLYSVYVNTMGLKFRQLLWFIISCLTFTGRTVTEYLV	120
Qy	121	SEGVWIRTPPAYRPPNAPILSTLPETTVVRRPGSRPRRTSPRRRRSSQSR	180
Db	121	SEGVWIRTPPAYRPPNAPILSTLPETTVVRRPGSRPRRTSPRRRRSSQSR	180
Qy	181	SQC 183	
Db	181	SQC 183	

```

RESULT 4
US-09-848-616-99
; Sequence 99, Application US/09848616
; Publication NO. US20030054010A1
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/09/848,616
; CURRENT FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-848-616-99

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Query Match	98.5%	Score 956;	DB 11;	Length 183;
Best Local Similarity	98.9%;	Pred. No. 1.5e-86;		
Matches 181;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MDIDPYKEFGATVELLISFLPSDFPSPVRDLDDTASALYREALSEPHCSPHHTALRAIL	60	
Db	1	MDIDPYKEFGATVELLISFLPSDFPSPVRDLDDTASALYREALSEPHCSPHHTALRAIL	60	
QY	61	CWGELMTLATWGVGNLEDPASRDLVSYVNTNGLKFRQLLWFIHSCILTTGTEVTIEVLY	120	
Db	61	CWGELMTLATWGVGNLEDPASRDLVSYVNTNGLKFRQLLWFIHSCILTTGTEVTIEVLY	120	
QY	121	SFGVWLTPTPAYPPNPAPILSTLPETVTVRRPGSPRRRTPSPPRRRSQSPRRRSQSRE	180	
Db	121	SFGVWLTPTPAYPPNPAPILSTLPETVTVRRPGSPRRRTPSPPRRRSQSPRRRSQSRE	180	
QY	181	SQC	183	
Db	181	SOC	183	

```

/ REGISTRATION NUMBER: 29,301
/ REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)655-1500
/ TELEFAX: (312)655-1501
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 183 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-386-591-38
/
Query Match 98.5%; Score 956; DB 11;
Best Local Similarity 98.9%; Pred. No. 1.5e-86;
Matches 181; Conservative 0; Mismatches 2;

```

QY 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
Db 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 7

US-10-243-739-39  
; Sequence 39, Application US/10243739  
; Publication No. US20030091593A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F.  
; APPLICANT: Storni, Tazio  
; APPLICANT: Lechner, Franziska  
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of  
; FILE REFERENCE: 1700.0210001  
; CURRENT APPLICATION NUMBER: US/10/243,739  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 60/318,967  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-10-243-739-39

Query Match 98.5%; Score 956; DB 15; Length 183;  
Best Local Similarity 98.9%; Pred. No. 1.5e-86;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
Db 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 8

US-10-244-065-39  
; Sequence 39, Application US/10244065  
; Publication No. US20030099668A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F.  
; APPLICANT: Storni, Tazio  
; APPLICANT: Maurer, Patrick  
; APPLICANT: Tissot, Alain  
; APPLICANT: Schwarz, Katrin  
; APPLICANT: Meijerink, Edwin  
; APPLICANT: Lipowsky, Gerard

; APPLICANT: Pumpens, Paul  
; APPLICANT: Cielens, Indulis  
; APPLICANT: Renhofa, Regina  
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Part  
; FILE REFERENCE: 1700.0220001  
; CURRENT APPLICATION NUMBER: US/10/244,065  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 60/374,145  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 60/318,994  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-10-244-065-39

Query Match 98.5%; Score 956; DB 15; Length 183;  
Best Local Similarity 98.9%; Pred. No. 1.5e-86;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
Db 1 MDIDPYKFGATVVELLSFLPSDFPSVROLDDTASALYREALSPHCSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
Db 61 CWGELMTLATWGVNLEDPASDLVSVYNTNMGKLFROLLWFHISCLTFGTETVIELV 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 9

US-09-929-955-11  
; Sequence 11, Application US/09929955  
; Patent No. US20020136740A1  
; GENERAL INFORMATION:  
; APPLICANT: Matti Sallberg  
; APPLICANT: Catharina Hultgren  
; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND  
; FILE REFERENCE: TRIPEP.23AUS2  
; CURRENT APPLICATION NUMBER: US/09/929,955  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/705,547  
; PRIOR FILING DATE: 2000-11-03  
; PRIOR APPLICATION NUMBER: 60/229,175  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: 60/225,767  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hepatitis B virus C antigen and e antigen  
; OTHER INFORMATION: (HBCag/HBeAg) sequence  
US-09-929-955-11

Query Match 98.5%; Score 956; DB 10; Length 212;  
Best Local Similarity 98.9%; Pred. No. 1.8e-86;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 89  
 |||||  
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
 |||||  
 Db 90 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 149  
 |||||  
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
 |||||  
 Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
 |||||  
 Qy 181 SQC 183  
 |||||  
 Db 210 SQC 212

## RESULT 10

US-10-104-966-11  
 ; Sequence 11, Application US/10104966  
 ; Publication No. US20020155124A1

## GENERAL INFORMATION:

; APPLICANT: Matti Sallberg  
 ; APPLICANT: Catharina Hultgren  
 ; TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND  
 ; FILE REFERENCE: TRIPEP.23AUSC1  
 ; CURRENT APPLICATION NUMBER: US/10/104,966  
 ; CURRENT FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: 09/705,547  
 ; PRIOR FILING DATE: 2000-11-03  
 ; PRIOR APPLICATION NUMBER: 60/229,175  
 ; PRIOR FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 212

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hepatitis B virus C antigen and e antigen

; OTHER INFORMATION: (HBCAg/HBeAg) sequence

US-10-104-966-11

Query Match 98.5%; Score 956; DB 14; Length 212;  
 Best Local Similarity 98.9%; Pred. No. 1.8e-86;  
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Db 30 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 89  
 |||||  
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
 |||||  
 Db 90 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 149  
 |||||  
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
 |||||  
 Db 150 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 209  
 |||||  
 Qy 181 SQC 183  
 |||||  
 Db 210 SQC 212

## RESULT 11

US-09-848-616-102  
 ; Sequence 102, Application US/09848616  
 ; Publication No. US20030054010A1

## GENERAL INFORMATION:

; APPLICANT: Sebbel, Peter

; APPLICANT: Dunant, Nicolas

; APPLICANT: Bachmann, Martin  
 ; APPLICANT: Tissot, Alain  
 ; APPLICANT: Lechner, Franziska  
 ; TITLE OF INVENTION: Molecular Antigen Array  
 ; FILE REFERENCE: 1700.0180002  
 ; CURRENT APPLICATION NUMBER: US/09/848,616  
 ; CURRENT FILING DATE: 2001-05-05  
 ; NUMBER OF SEQ ID NOS: 186  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 102  
 ; LENGTH: 183  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic  
 ; OTHER INFORMATION: human Hepatitis B construct  
 ; US-09-848-616-102

Query Match 98.2%; Score 954; DB 11; Length 183;  
 Best Local Similarity 98.4%; Pred. No. 2.4e-86;  
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
 |||||  
 Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
 |||||  
 Qy 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
 |||||  
 Db 121 SFGWIRTPPAYRPPNAPILSTLPTTVVRRGSPRRRTSPRRRSQSPRRRSQSRE 180  
 |||||  
 Qy 181 SQC 183  
 |||||  
 Db 181 SQC 183

## RESULT 12

US-10-243-739-42  
 ; Sequence 42, Application US/10243739  
 ; Publication No. US20030091593A1

## GENERAL INFORMATION:

; APPLICANT: Bachmann, Martin F.  
 ; APPLICANT: Storni, Tazio  
 ; APPLICANT: Lechner, Franziska  
 ; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement  
 ; FILE REFERENCE: 1700.0210001  
 ; CURRENT APPLICATION NUMBER: US/10/243,739  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 60/318,967  
 ; PRIOR FILING DATE: 2001-09-14  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 42

; LENGTH: 183

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic human Hepatitis B virus core protein gene

US-10-243-739-42

Query Match 98.2%; Score 954; DB 15; Length 183;  
 Best Local Similarity 98.4%; Pred. No. 2.4e-86;  
 Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Db 1 MDIDPYKEFGATVELLSFLPSDFPVSVDLDDTASALYREALAESPEHCSPHHTALRQAIL 60  
 |||||  
 Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGKFRQLLWFHISCLTFGTETVIEYLV 120  
 |||||

Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 13

US-10-244-065-42  
; Sequence 42, Application US/10244065  
; Publication No. US20030099668A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F.  
; APPLICANT: Storni, Tazio  
; APPLICANT: Maurer, Patrick  
; APPLICANT: Tissot, Alain  
; APPLICANT: Schwarz, Katrin  
; APPLICANT: Meijerink, Edwin  
; APPLICANT: Lipowsky, Gerard  
; APPLICANT: Pumps, Paul  
; APPLICANT: Cielens, Indulis  
; APPLICANT: Renhofs, Regina  
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Partic  
; FILE REFERENCE: 1700.0220001  
; CURRENT APPLICATION NUMBER: US/10/244,065  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 60/374,145  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: 60/318,994  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 42  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic human Hepatitis B virus core protein gene  
US-10-244-065-42

Query Match 98.2%; Score 954; DB 15; Length 183;  
Best Local Similarity 98.4%; Pred. No. 2.4e-86;  
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 14

US-09-848-616-104  
; Sequence 104, Application US/09848616  
; Publication No. US20030054010A1  
; GENERAL INFORMATION:  
; APPLICANT: Sebbel, Peter

; APPLICANT: Dunant, Nicolas  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Tissot, Alain  
; APPLICANT: Lechner, Franziska  
; TITLE OF INVENTION: Molecular Antigen Array  
; FILE REFERENCE: 1700.0180002  
; CURRENT APPLICATION NUMBER: US/09/848,616  
; CURRENT FILING DATE: 2001-05-05  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-09-848-616-104

Query Match 98.1%; Score 953; DB 11; Length 183;  
Best Local Similarity 98.4%; Pred. No. 3e-86;  
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180  
QY 181 SQC 183  
Db 181 SQC 183

## RESULT 15

US-09-848-616-105  
; Sequence 105, Application US/09848616  
; Publication No. US20030054010A1  
; GENERAL INFORMATION:  
; APPLICANT: Sebbel, Peter  
; APPLICANT: Dunant, Nicolas  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Tissot, Alain  
; APPLICANT: Lechner, Franziska  
; TITLE OF INVENTION: Molecular Antigen Array  
; FILE REFERENCE: 1700.0180002  
; CURRENT APPLICATION NUMBER: US/09/848,616  
; CURRENT FILING DATE: 2001-05-05  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 105  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-09-848-616-105

Query Match 98.1%; Score 953; DB 11; Length 183;  
Best Local Similarity 98.4%; Pred. No. 3e-86;  
Matches 180; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRQAIL 60  
QY 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
Db 61 CWGELMTLATWGVNLEDPASRDLYVSVYNTNMGLKFRQLLWFHISCLTFGRETVEYL 120  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180

Db 121 SFGVWIRTPPAYRPPNAPILSTLETTVVRRGRSPRRRTFSPRRRSQSPRRRSQSR 180  
Qy 181 SQC 183  
Db 181 SQC 183

Search completed: August 6, 2003, 09:55:03  
Job time : 50 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2003, 09:42:19 ; Search time 29 Seconds  
(without alignments)  
266.996 Million cell updates/sec

Title: US-09-812-862-12

Perfect score: 971

Sequence: 1 MDIDPKFEGATVLLSLP.....RRRSQSPRRRSQSRSSQC 183

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*

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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	971	100.0	183	5	PCT-US96-10602-12
2	956	98.5	183	3	US-09-248-588-2
3	956	98.5	194	3	US-08-968-747-18
4	956	98.5	212	3	US-08-968-747-3
5	956	98.5	346	1	US-08-105-483-217
6	956	98.5	346	1	US-08-709-209-217
7	956	98.5	346	1	US-08-458-101-217
8	941	96.9	183	3	US-08-968-747-20
9	941	96.9	193	3	US-08-968-747-2
10	933	96.1	397	5	PCT-US96-10602-6
11	930.5	95.8	199	3	US-08-968-747-21
12	927	95.5	185	1	US-07-739-642-2
13	927	95.5	185	1	US-07-739-643-2
14	927	95.5	185	1	US-07-739-142-4
15	927	95.5	185	4	US-09-851-120-6
16	924	95.2	185	3	US-09-248-588-6
17	923	95.1	183	3	US-09-248-588-4
18	923	95.1	185	1	US-07-739-642-4
19	923	95.1	185	1	US-07-739-643-4
20	923	95.1	185	1	US-07-739-142-4
21	920	94.7	289	5	PCT-US96-10602-8
22	915	94.2	185	1	US-07-739-642-10
23	915	94.2	185	1	US-07-739-643-10
24	915	94.2	185	1	US-07-739-142-10
25	912	93.9	185	1	US-07-739-642-8
26	912	93.9	185	1	US-07-739-643-8
27	912	93.9	185	1	US-07-739-142-8

28	900	92.7	212	4	US-09-719-528A-4
29	880.5	90.7	211	6	5196194-13
30	872	89.8	351	5	PCT-US96-10602-4
31	787	81.1	159	3	US-08-445-585-3
32	772	79.5	214	1	US-07-739-642-12
33	772	79.5	214	1	US-07-739-643-12
34	772	79.5	214	1	US-07-739-142-12
35	767	79.0	214	1	US-07-739-642-6
36	767	79.0	214	1	US-07-739-643-6
37	767	79.0	214	1	US-07-739-142-6
38	764	78.7	154	3	US-08-968-747-1
39	764	78.7	155	3	US-08-968-747-17
40	764	78.7	161	3	US-08-968-747-19
41	672.5	69.3	188	3	US-09-248-588-7
42	671	69.1	217	3	US-09-248-588-9
43	616	63.4	346	5	PCT-US96-10602-2
44	192	19.8	39	3	US-08-968-747-5
45	173	17.8	305	3	US-09-248-588-11

## ALIGNMENTS

RESULT 1  
PCT-US96-10602-12  
; Sequence 12, Application PC/TUS9610602  
; GENERAL INFORMATION:  
; APPLICANT: The General Hospital Corporation  
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10602  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/017,814  
; FILING DATE: 20-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/282001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 183 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-10602-12

Query Match 100.0%; Score 971; DB 5; Length 183;  
Best Local Similarity 100.0%; Pred. No. 6.9e-100;  
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIDPKFEGATVLLSLPSPDFPVSRLDLDTASALYREALSEPHHCSPHHTALRQAIL 60  
|||||  
DB 1 MDIDPKFEGATVLLSLPSPDFPVSRLDLDTASALYREALSEPHHCSPHHTALRQAIL 60  
|||||

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QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 120
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DB 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 120
|||||
QY 121 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
DB 121 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
QY 181 SOC 183
|||
DB 181 SOC 183
|||

RESULT 2
US-09-248-588-2
; Sequence 2, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; FILE REFERENCE: SYN-101 4564/89529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-2

Query Match 98.5%; Score 956; DB 3; Length 183;
Best Local Similarity 98.9%; Pred. No. 3.2e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKRGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
DB 1 MDIDPYKRGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 120
|||||
DB 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 120
|||||
QY 121 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
DB 121 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
QY 181 SOC 183
|||
DB 181 SOC 183
|||

RESULT 3
US-08-968-747-18
; Sequence 18, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 08472/705001
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-18

Query Match 98.5%; Score 956; DB 3; Length 194;
Best Local Similarity 98.9%; Pred. No. 3.4e-98;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDIDPYKRGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 60
|||||
DB 12 MDIDPYKRGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAIL 71
|||||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 120
|||||
DB 72 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKFRQLLWPHISCLFTGTVIEYLV 131
|||||
QY 121 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 180
|||||
DB 132 SFGWIRTPPAYPPNAPILSTLPTVTVRRGSRPRRTTPSPRRRSQSPRRRSQSR 191
|||||
QY 181 SOC 183
|||
DB 192 SOC 194
|||

RESULT 4
US-08-968-747-3
; Sequence 3, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 08472/705001
; MEDIUM TYPE: Floppy disk
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TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 212 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-968-747-3

Query Match 98.5%; Score 956; DB 3; Length 212;  
Best Local Similarity 98.9%; Pred. No. 3.9e-98;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRAIL 60  
DB 30 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRAIL 89  
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120  
DB 90 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 149  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGSRPRRTSPRRRSQSPRRRSQSR 180  
DB 150 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGSRPRRTSPRRRSQSPRRRSQSR 209  
QY 181 SQC 183  
DB 210 SQC 212

RESULT 5  
US-08-105-483-217  
Sequence 217, Application US/08105483  
Patent No. 5494807  
GENERAL INFORMATION:  
APPLICANT: Paolletti, Enzo  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 462  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/105.483  
FILING DATE: 12-AUG-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
US-08-105-483-217  
Query Match 98.5%; Score 956; DB 1; Length 346;  
Best Local Similarity 98.9%; Pred. No. 7.7e-98;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRAIL 60  
DB 164 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALRAIL 223  
QY 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 120  
DB 224 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGLKFRQLLWFHISCLTFGTETVIELV 283  
QY 121 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGSRPRRTSPRRRSQSPRRRSQSR 180  
DB 284 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGSRPRRTSPRRRSQSPRRRSQSR 343  
QY 181 SQC 183  
DB 344 SQC 346

RESULT 6  
US-08-709-209-217  
Sequence 217, Application US/08709209  
Patent No. 5762938  
GENERAL INFORMATION:  
APPLICANT: Paolletti, Enzo  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 462  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/709,209  
FILING DATE: 21-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/105,483  
FILING DATE: 12-AUG-1993  
APPLICATION NUMBER: US 07/847,951  
FILING DATE: 06-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-709-209-217

Query Match 98.5%; Score 956; DB 1; Length 346;  
Best Local Similarity 98.9%; Pred. No. 7.7e-98;  
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MDIDYKKEGATVELLSFLPSDFTPPSVRDLLDTASALYREALSPHCSPHHTALQAIL	60
Db	164	MDIDYKKEGATVELLSFLPSDFTPPSVRDLLDTASALYREALSPHCSPHHTALQAIL	223
Qy	61	CWGLMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV	120
Db	224	CWGLMTLATWGVNLEDPASRDLVSVYNTNMGKFKRQLLWFHISCLTFGTETVIEYLV	283
Qy	121	SGVWIRTPPAYRPPNAPILSTLPTTIVWRPGSPRRRTTPSPRRRSQSPRRRSQSRE	180
Db	284	SGVWIRTPPAYRPPNAPILSTLPTTIVWRPGSPRRRTTPSPRRRSQSPRRRSQSRE	343
Qy	181	SOC 183	
Db	344	SOC 346	

RESULT 7  
US-08-458-101-217  
US: Sequence 217, Application US/08458101  
Patent No. 5766599  
GENERAL INFORMATION:  
APPLICANT: Paolletti, Enzo  
APPLICANT: Perkus, Marlon E.  
APPLICANT: Taylor, Jill  
APPLICANT: Tartaglia, James  
APPLICANT: No. 5766599ton, Elizabeth K.  
APPLICANT: Riviere, Michel  
APPLICANT: de Taisne, Charles  
APPLICANT: Limbach, Keith J.  
APPLICANT: Johnson, Gerard P.  
APPLICANT: Pincus, Steven E.  
APPLICANT: Cox, William I.  
APPLICANT: Audonnet, Jean-Christophe Francis  
APPLICANT: Gettig, Russell Robert  
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
TITLE OF INVENTION: STRAIN  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William S. Frommer  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,101  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2740  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 217:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 346 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-458-101-217

Matches	181:	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	MDIDPYKEFGATV	ELL	SFLP	SDFFPSVR	LLD	TASALYREALESPHCSPHHTALRQAIL	60	
Db	164	MDIDPYKEFGATV	ELL	SFLP	SDFFPSVR	LLD	TASALYREALESPHCSPHHTALRQAIL	223	
Qy	61	CWGLMTLATWVG	NLEDDPAS	RDLV	SVYNTNGLK	FQRQLLWFHHSCLTTGTTETVIEYL	120		
Db	224	CWGLMTLATWVG	NLEDDPAS	RDLV	SVYNTNGLK	FQRQLLWFHHSCLTTGTTETVIEYL	283		
Qy	121	SFGWIIRTPPAY	PPNPAPILSTLP	ETTVRRPGRS	PRRRTGPS	PRRRRSQS	PRRRRSQS	180	
Db	284	SFGWIIRTPPAY	PPNPAPILSTLP	ETTVRRPGRS	PRRRTGPS	PRRRRSQS	PRRRRSQS	343	
Qy	181	QC	183						
Db	344	QC	346						
RESULT 8									
US-08-968-747-20									
; Sequence 20, Application US/08968747.									
; Patent No. 6060595									
; GENERAL INFORMATION:									
; APPLICANT: Scaglioni et al.									
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION									
; NUMBER OF SEQUENCES: 21									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Fish & Richardson P.C.									
; STREET: 225 Franklin Street									
; CITY: Boston									
; STATE: MA									
; COUNTRY: USA									
; ZIP: 02110-2804									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: Windows									
; SOFTWARE: PatentIn Release #1.0, version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/968,747									
; FILING DATE: 03-SEP-1997									
; CLASSIFICATION: 435									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Fraser, Janis K.									
; REGISTRATION NUMBER: 34,819									
; REFERENCE/DOCKET NUMBER: 08472/705001									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 617/542-5070									
; TELEFAX: 617/542-8906									
; TELEX: 200154									
; INFORMATION FOR SEQ ID NO: 20:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 183 amino acids									
; TYPE: amino acid									
; STRANDEDNESS: not relevant									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
US-08-968-747-20									

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Db 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
181 SQC 183
Db 181 SQC 183

RESULT 9
US-08-968-747-2
; Sequence 2, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-747-2

Query Match 96.9%; Score 941; DB 3; Length 193;
Best Local Similarity 97.8%; Pred. No. 1.6e-96;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLSPDFPSVDRLLDTASALYREALSPHCHSPHHTALQAIL 60
Db 11 MDIDPYKEFGATVELLSFLSPDFPSVDRLLDTASALYREALSPHCHSPHHTALQAIL 70

Qy 61 CWGELMTLATWGVGNLEDPASRDVLVSYVNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
Db 71 CWGELMTLATWGVGNLEDPASRDVLVSYVNTNMGKFRQLLWFIHISCLTGTETVIEYLV 130

Qy 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 180
Db 131 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSRE 190

Qy 181 SQC 183
Db 191 SQC 193

RESULT 10
PCT-US96-10602-6
; Sequence 6, Application PC/TUS9610602
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; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/282001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10602-6

Query Match 96.1%; Score 933; DB 5; Length 397;
Best Local Similarity 98.9%; Pred. No. 3.3e-95;
Matches 177; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDIDPYKEFGATVELLSFLSPDFPSVDRLLDTASALYREALSPHCHSPHHTALQAIL 60
Db 1 MDIDPYKEFGATVELLSFLSPDFPSVDRLLDTASALYREALSPHCHSPHHTALQAIL 60

Qy 61 CWGELMTLATWGVGNLEDPASRDVLVSYVNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120
Db 61 CWGELMTLATWGVGNLEDPASRDVLVSYVNTNMGKFRQLLWFIHISCLTGTETVIEYLV 120

Qy 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSQR 179
Db 121 SFGWIRTPPAYPPNAPILSTLPTTAVRRGRSPRRTPSPRRRSQSPRRRSQSQR 179

RESULT 11
US-08-968-747-21
; Sequence 21, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,747  
FILING DATE: 03-SEP-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08472/705001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
OS-08-968-747-21

RESULT 12  
US-07-739-642-2  
; Sequence 2, Application US/07739642  
Patent No. 5173427  
GENERAL INFORMATION:  
APPLICANT: Mallonee,, Richard L.  
; TITLE OF INVENTION: Vectors And Hosts With Increased  
; TITLE OF INVENTION: Expression Of HBCaG  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Richard R. Rodrick  
; STREET: 1 Becton Drive  
; CITY: Franklin Lakes  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07417-1880  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07739,642  
; FILING DATE: 19910801  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stierwalt,, Brian K.  
; REGISTRATION NUMBER: 33,213

```

; ; REFERENCE/DOCKET NUMBER: P-2272
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 201-848-5317
; ; TELEFAX: 201-848-9228
; ; INFORMATION FOR SEQ ID NO: 2:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 185 amino acids
; ; TYPE: AMINO ACID
; ; TOPOLOGY: linear
; ;
US-07-739-642-2

Query Match          95.5%; Score
Best Local Similarity 95.7%; Pred.
Matches 177; Conservative 2; Mismatches 18

QY      1 MDIDPYKFGATGAYELLISFLPSDFPP
Db      1 MDIDPYKFGATGAYELLISFLPSDFPP
QY      61 CWGELMTLATWGVGNLEDPASRDVLV
Db      61 CWGELMTLATWGVGNLEDPASRDVLV
QY      121 SGFGWLRTPPAYRPPNAPILSTLPE
Db      121 SGFGWLRTPPAYRPPNAPILSTLPE
QY      179 RESQC 183
Db      181 RESQC 185

```

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RESULT 13
US-07-739-643-2
; Sequence 2, Application US/07739643
; Patent No. 5175094
; GENERAL INFORMATION:
; APPLICANT: Mallonee,, Richard L.
; TITLE OF INVENTION: Increased Expression of HbAa9
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Rodrick
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07739,643
; FILING DATE: 19910801
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stierwalt,, Brian K.
; REGISTRATION NUMBER: 33,213
; REFERENCE/DOCKET NUMBER: P-2090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-848-5317
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-739-643-2

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Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60  
Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180  
Qy 179 RESQC 183  
Db 181 RESQC 185

## RESULT 14

S-07-739-142-2

Sequence 2, Application US/07739142

Patent No. 5175272

GENERAL INFORMATION:

APPLICANT: Mallonee, Richard L.

TITLE OF INVENTION: DNA Sequences With Increased Expression

TITLE OF INVENTION: of HbcAg

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard R. Rodrick

STREET: 1 Becton Drive

CITY: Franklin Lakes

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07417-1880

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07739,142

FILING DATE: 19910801

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stierwalt, Brian K.

REGISTRATION NUMBER: 33,213

REFERENCE/DOCKET NUMBER: P-2271

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-848-5317

TELEFAX: 201-848-9228

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-739-142-2

Query Match 95.5%; Score 927; DB 1; Length 185;

Best Local Similarity 95.7%; Pred. No. 5.3e-95;

Matches 177; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60  
Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 179 RESQC 183  
Db 181 RESQC 185

## RESULT 15

US-09-851-120-6

Sequence 6, Application US/098511120

Patent No. 6479282

GENERAL INFORMATION:

APPLICANT: LETOURNEUR, Odile

TITLE OF INVENTION: WATELET, Benedicte

FILE REFERENCE: 109455

CURRENT APPLICATION NUMBER: US/09/851,120

CURRENT FILING DATE: 2001-09-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 6

LENGTH: 185

TYPE: PRT

ORGANISM: HBV

US-09-851-120-6

Query Match 95.5%; Score 927; DB 4; Length 185;

Best Local Similarity 95.7%; Pred. No. 5.3e-95;

Matches 177; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60  
Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHHTALQAIL 60

Qy 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Db 61 CWGELMTLATWGVNLEDPASRDVLVSVYNTNMGLKQRLWFIHISCLTFGTETVIEYLV 120  
Qy 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRR--PCRSPPRRTPSPRRRSQSPRRRSQS 178  
Db 121 SFGVWIRTPPAYRPPNAPILSTLPTETTVVRRDRGRSPRRTPSPRRRSQSPRRRSQS 180

Qy 179 RESQC 183  
Db 181 RESQC 185

Search completed: August 6, 2003, 09:47:18

Job time : 30 secs

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